1200 575000

SEQUENCE LISTING

<110> SUNTORY LIMITED

- <130> SU0411
- <140> PCT/JP2004/0146696
- <141> 2004-09-24
- <150> JP 2003-341313
- <151> 2003-09-30
- <150> JP 2003-432383
- <151> 2003-12-26
- <160> 79
- <170> PatentIn Ver. 2.1
- <210> 1
- <211> 506
- <212> PRT
- <213> Sesamum indicum
- <220>
- <223> SiP189
- <400> 1
- Met Glu Ala Glu Met Leu Tyr Ser Ala Leu Ala Leu Thr Phe Ala Ile 1 5 10 15
- Phe Met Val Tyr Arg Ile Leu Ser Asn Ser Gln Asp Lys Arg Ser Leu 20 25 30
- Thr Lys Leu Pro Pro Ser Pro Pro Gly Trp Leu Pro Val Ile Gly His
 35 40 45
- Ala His Leu Met Lys Asn Leu Leu His Arg Thr Leu Tyr Asp Phe Ser 50 55 60
- Gln Lys Leu Gly Pro Ile Phe Ser Ile Arg Phe Gly Ser Arg Leu Val 65 70 75 80
- Val Val Val Ser Ser Ser Leu Val Glu Glu Cys Phe Thr Lys Tyr 85 90 95
- Asp Ile Val Leu Ala Asn Arg Pro Gln Ala Ser Val Asp Arg Arg Ser 100 105 110
- Leu Gly Phe Ser Thr Thr Ser Val Ile Gly Ala Pro Tyr Gly Asp His
 115 120 125
- Trp Arg Asn Leu Arg Lys Leu Cys Asp Leu Glu Val Phe Ala Pro Thr 130 135 140

Arg Leu Ala Ser Phe Leu Ser Ile Arg Leu Asp Glu Arg Asp Arg Met Ile Ser Ala Leu Tyr Lys Ile Ser Ser Ala Gly Phe Ala Lys Val Asn Leu Glu Ala Lys Ile Val Glu Leu Thr Phe Asn Asn Ile Met Arg Met 180 185 Val Ala Ala Lys Arg Tyr Tyr Gly Glu Glu Ala Glu Asp Asp Glu Glu 200 Ala Lys Arg Phe Arg Asp Leu Thr Lys Glu Ala Leu Glu Leu Thr Ser 210 215 Ala Ser Asn Pro Gly Glu Ile Phe Pro Ile Leu Arg Trp Leu Gly Cys 230 Asn Gly Leu Glu Lys Lys Leu Ala Val His Ser Arg Lys Thr Asp Glu 245 250 Phe Met Gln Gly Leu Leu Asp Glu His Arg Arg Gly Glu Arg Gln Asn 260 Thr Met Val Asp His Leu Leu Ser Leu Gln Glu Ser Gln Pro Glu Tyr 280 Tyr Thr Asp Glu Ile Ile Thr Gly Leu Ile Val Ala Leu Ile Ile Ala 290 295 Gly Thr Asp Ala Ser Val Val Thr Thr Glu Trp Ala Met Ser Leu Leu 305 315 320 Leu Asn His Pro Lys Val Leu Glu Lys Ala Arg Lys Glu Leu Asp Thr Leu Val Gly His Glu Arg Met Val Asp Glu His Asp Leu Pro Lys Leu 340 Arg Tyr Leu His Cys Ile Val Leu Glu Thr Leu Arg Leu Phe Pro Ser 360 Val Pro Thr Leu Val Pro His Glu Pro Ser Glu Asp Cys Lys Ile Gly 370 375 Gly Tyr Asn Val Pro Lys Gly Thr Met Val Leu Val Asn Ala Trp Ala 390 400 Ile His Arg Asp Pro Lys Val Trp Asp Asp Pro Leu Ser Phe Lys Pro 405 410 Asp Arg Phe Glu Ile Met Glu Val Glu Thr His Lys Leu Leu Pro Phe 420 Gly Met Gly Arg Arg Ala Cys Pro Gly Ala Gly Leu Ala Gln Lys Phe 435 440

Val Gly Leu Ala Leu Gly Ser Leu Ile Gln Cys Phe Asp Trp Glu Arq 455 Thr Ser Pro Glu Lys Ile Asp Leu Asn Glu Gly Ser Gly Ile Thr Leu 470 Pro Lys Ala Lys Thr Leu Glu Ala Met Cys Lys Pro Arg His Val Met 485 490 Glu Lys Val Leu Arg Gln Val Ser Asn Val 500 <210> 2 <211> 1518 <212> DNA <213> Sesamum indicum <220> <223> SiP189 <400> 2 atggaagctg aaatgctata ttcagctctc gctctcacct tcgccatatt catggtttac 60 agaattettt etaattegea ggacaagege ageetgacta agetgeetee qaqeeeqeee 120 ggttggctgc cggtgatcgg ccacgctcat ctcatgaaaa atctcctcca tagaacacta 180 tacgacttct cccagaaact gggacccata ttttccatcc ggttcgggtc gcgcctcgtg 240 gtggtggtgt cctcctcctc cctggtggag gaatgtttca ccaagtatga cattgtcttg 300 gcaaatcgcc ctcaggcttc tgttgaccgg cgctcacttg ggttcagcac caccagcgta 360 atcggggccc cgtacgggga ccattggcgc aacctgcgaa agttgtgcga tcttgaagta 420 ttcgccccga cccgtctcgc ctcgttttta tccatcaggc ttgacgagag ggaccgcatg 480 atttccgcgt tatacaaaat ctcgtccgcc ggtttcgcga aggtgaattt ggaagcgaag 540 attgtggagc tgacgtttaa taacataatg aggatggtgg cggcgaagag atactatggg 600 gaggaggcgg aggacgacga ggaggcgaag aggttcaggg acctgacgaa ggaggctttg 660 gagttgacga gcgcttccaa tcctggtgag atatttccaa tattgcggtg gcttggttgc 720 aatgggctgg agaagaagct ggctgttcac tcgcggaaga cggatgagtt catgcaaggg 780 ctgctggacg aacaccgacg gggcgagcgc cagaacacca tggttgatca tttqctttcq 840 ttgcaggaat ctcaacctga gtactacact gatgaaatca tcactggcct catagttgca 900 ttgataattg cgggaacgga tgcatcggtt gtaactacag aatgggcgat gtccctttta 960 ctaaatcatc ccaaagtact tgaaaaggct agaaaagaac tggacactct agtaggacac 1020 gaacgcatgg ttgatgaaca cgatctcccc aaactacgtt accttcactg catagtcttg 1080 gagaccttaa ggttattccc ttctgttcca actttggtgc cacacgaacc atcagaggat 1140 tgtaaaattg ggggatacaa tgtccccaag gggacaatgg tattagtgaa tgcttgggca 1200 atacaccgag accccaaggt gtgggacgac cccttgagct ttaagcccga caggtttgag 1260 ataatggaag tggagacaca caagttgttg ccgttcggaa tgggcaggag agcgtgtcct 1320 ggagctggac tggcgcagaa gtttgtgggg ttggctttgg ggtcgctgat tcagtgtttc 1380 gactgggaga gaacgagtcc cgagaaaatt gacttgaacg aaggttctgg gataaccttg 1440 cctaaagcta agacgttgga agccatgtgc aaacctagac atgtcatgga aaaagttctt 1500 cgtcaggttt ccaacgtt <210> 3 <211> 21 <212> DNA <213> Artificial Sequence

<223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, Si18SrRNA-FW	
<400> 3 tatgcttgtc tcaaagatta a	21
<210> 4 <211> 21 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, Sil8SrRNA-RV	
<400> 4 aacatctaag ggcatcacag a	21
<210> 5 <211> 24 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP90A-FW	
<400> 5 ttttccgatg aagagattgt tgac	24
<210> 6 <211> 18 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP90A-RV	
<400> 6 tgccatctcc aagggttg	18
<210> 7 <211> 24 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP72B-FW	
<400> 7 cttaatgttc aaatgataat ggat	24

```
<210> 8
<211> 18
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Artificially
      Synthesized Primer Sequence, CYP72B-RV
<400> 8
gtaaatcgtt cagggttg
                                                                    18
<210> 9
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Artificially
      Synthesized Primer Sequence, CYP71B-FW
<400> 9
ttcaccactg atcatctcaa agga
                                                                    24
<210> 10
<211> 18
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Artificially
      Synthesized Primer Sequence, CYP71B-RV
<400> 10
agaaacctgt cagggtta
                                                                    18
<210> 11
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Artificially
      Synthesized Primer Sequence, CYP84A-FW
<400> 11
cttacccgtg acaatatcaa agca
                                                                    24
<210> 12
<211> 18
<212> DNA
```

•

<213>	Artificial Sequence	
<220>		
	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP84A-RV	
<400>	12	
aaaaa	cctcg atggtcta	18
<210>	13	
<211>	24	
<212>		
<213>	Artificial Sequence	
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP96A-FW	
<400>	12	
	gata agtteeteag ggae	24
agccai	syaca ayuuduu gyad	24
<210>	14	
<211>		
<212>	DNA	
	Artificial Sequence	
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP96A-RV	
<400>		
atccai	cctct ctggcttg	18
<210>	15	
<211>		
<212>		
	Artificial Sequence	
<220>		
<223>	Description of Artificial Sequence: Artificially	
	Synthesized Primer Sequence, CYP710A-FW	
<400>		
tccgaa	agacg aagccatcgg cggt	24
.0.1.0	16	
<210>		
<211>		
<212>		
\413 >	Artificial Sequence	
<220>		
	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP710A-RV	

<400> 16 ctaaaccggt ccggatcg	18
<210> 17 <211> 24 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP86A-FW	
<400> 17 cgcgtggcgc tcaacttcat ccta	24
<210> 18 <211> 18 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP86A-RV	
<400> 18 atccatctct ctggtttg	18
<210> 19 <211> 24 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP74-FW	
<400> 19 cgagaagaag ctactcacaa tctt	24
<210> 20 <211> 18 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP74-RV	
<400> 20 acgaatctct ccggcaca	18

<210><211><212><213>	25	
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP75B-FW	
<400> ttaaco	21 ggata ctgagattaa agcct	25
<210><211><212><213>	18	
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP75B-RV	
<400> aagaat	22 cctct cgggttta	18
<210><211><211><212><213>	24	
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP79F-FW	
<400> gtcaca	23 accag acgaaatcaa agct	24
<210><211><212><213>	18	
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP79F-RV	
<400> aggtga	24 acgct ccggtttg	18
<210><211><211><212><213>	24	

<220> <223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP81D-FW <400> 25 tacatggacc gcatcatcaa agga 24 <210> 26 <211> 18 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP81D-RV <400> 26 tcgaacctct ctggcttg 18 <210> 27 <211> 24 <212> DNA <213> Artificial Sequence <223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP705A-FW <400> 27 catatcaagt cgcttctcac ggta 24 <210> 28 <211> 18 <212> DNA <213> Artificial Sequence <223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP705A-RV <400> 28 agaaacctct ctggttta 18 <210> 29 <211> 24 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP83A-FW <400> 29

•

tttactgatg ataatgtcaa agcc	24
<210> 30	
<211> 18 <212> DNA	
<212> DNA <213> Artificial Sequence	
(213) Arctificial Sequence	
<220>	
<pre><223> Description of Artificial Sequence: Artificially</pre>	
Synthesized Primer Sequence, CYP83A-RV	
<400> 30	
agaaacctct cgggccta	18
<210> 31	
<211> 21	
<212> DNA	
<213> Artificial Sequence	
.000	
<220>	
<223> Description of Artificial Sequence: Artificially	
Synthesized Primer Sequence, SiP168-FW	
<400> 31	
tttcccttgt tctcctactc t	21
	21
<210> 32	
<211> 21	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Artificially	
Synthesized Primer Sequence, SiP168-RV	
<400> 32	
	2.1
aaataatgat agctaaattt t	21
<210> 33	
<211> 21	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Artificially	
Synthesized Primer Sequence, SiP189-FW	
.400. 22	
<400> 33	
tcgtttttat ccatcaggct t	21
<210> 34	
<211> 21	

<212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, SiP189-RV	
<400> 34 caaacgttgg aaacctgacg a	21
<210> 35 <211> 21 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, SiP236-FW	
<400> 35 ggatgttctg tggaagttaa a	21
<210> 36 <211> 21 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, SiP236-RV	
<400> 36 atctaagttt catgcagttt t	21
<210> 37 <211> 21 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, SiP249-FW	
<400> 37 ctaagcttca aaatgtcgat a	21
<210> 38 <211> 21 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Artificially	

Synthesized Primer Sequence, SiP249-RV

<400> 38 ccaacttact tattacagat a	21
<210> 39 <211> 21 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, SiP288-FW	
<400> 39 aaaatggtgg gaattgtgta t	21
<210> 40 <211> 19 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, SiP288-RV	
<400> 40 tacatctcaa tttttctta	19
<210> 41 <211> 32 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, GR-SiP168-RV	
<400> 41 cacgatcctg gagatttccg gggaggatac aa	32
<210> 42 <211> 18 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, GR-SiP168-Nest-RV	
<400> 42 gtaggttttg gagagttt	18

<210>	43	
<211>	31	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
	Degraphion of Ambificial Company Autificial	
<223>	Description of Artificial Sequence: Artificially	
	Synthesized Primer Sequence, GR-SiP189-RV	
<400>	43	
ctcgto	egtec teegeeteet eeceatagta t	31
<210>	44	
<211>	21	
<212>		
<213>	Artificial Sequence	
<220>		
<223>	Description of Artificial Sequence: Artificially	
	Synthesized Primer Sequence, GR-SiP189-Nest-RV	
<400>	44	
accato	cctca ttatgttatt a	21
	•	
<210>	45	
<211>		
<212>		
<213>	Artificial Sequence	
<220>		
<223>	Description of Artificial Sequence: Artificially	
	Synthesized Primer Sequence, GR-SiP236-RV	
<400>	45	
ccaqqa	agaga gttgttgctg ttgtgtct	28
	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	20
<210>	46	
<211>		
<212>		
<213>	Artificial Sequence	
<220>		
<223>	Description of Artificial Sequence: Artificially	
	Synthesized Primer Sequence, GR-SiP236-Nest-RV	
<400>	46	
tataaa	agctt attgttat	18
<210>	47	
<211>		
<212>		
	Artificial Sequence	
~~±3>	Profit pedacine	

<220> <223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, SiP168-BamHl-FW <400> 47 ggatccaaaa gagcaaatta tggatctact act 33 <210> 48 <211> 33 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, SiP168-Xhol-RV <400> 48 ctcgagaagg gaaaataatg atagctaaat ttt 33 <210> 49 <211> 30 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, SiP189-BamHl-FW <400> 49 ggatcctttt cagccaacat ggaagctgaa 30 <210> 50 <211> 33 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, SiP189-Xhol-RV <400> 50 ctcgagaaaa agagcatcat ttaatcatac act 33 <210> 51 <211> 35 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, SiP236-BamH1-FW

```
<400> 51
ggatccttca cttcacttca ttgctcaatg gcaaa
                                                                  35
<210> 52
<211> 33
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Artificially
     Synthesized Primer Sequence, SiP236-Xhol-RV
<400> 52
ctcgagaaca gctgagaccc cacagcaatc taa
                                                                  33
<210> 53
<211> 1503
<212> DNA
<213> Sesamum indicum
<220>
<223> SiP249
<400> 53
atgtcgatac ctctccttat ctctctcta ttaatcatcc ttgttttcct actagtccga 60
cgacgccgca acagcccggc tggtcgaaaa ctccggcgtc ctccggggcc tcctqqcctt 120
cccttcctcg ggaacttgct ccaatacaac ccctccgatc tccatctccg cctgacaaaa 180
ctctcagaaa agtacggccc gcttatgtac atgacgttcg tcggaaagcc cgtggttgtg 240
atttcatcgg cccgagtggc caaagaggct ttgaaqtaca atqaccttqc attttcgagc 300
aggeetteta ceattgeate gegeaaagtg gettacaaca acagtgacat etceatgtea 360
ccgtacacag agtactggag agaactgcgg aaaatggtcg ttcttcgcct ctttacqqtc 420
aaacaagtga actctttccg ccctgctcga gaagaagaag tggcccgcat ggtgaaagag 480
atttccagac gggccaacgc gcatcagccc gttaacatta atgaaatagc gttgtcgttg 540
tcgagcagga tgatatctag gtttgcactg gggaagaggt acgacgagga gaacgggccg 600
gaaaagagga ggttcgacag gattctgcag ctgcttcagt tggtgtcggt ggaaattttc 660
tttggtgatt attctccatg gctgggctgg attgacagac tgtgtggtaa ggtttctcag 720
cttgagaagg cgttcaagga tttggattca ttgtatgaag agatgatcgc ggagcatctg 780
agcccgaata ggcccgagtc tatgaacgga gacattcttg atatgctaat tcagatgaaa 840
gaagatcggt cgtcgacggt tcaaattgat tgggatcata tcaagggcgt actcatgaac 900
atgttcgtag ccggaacaga cacaactgca gctacaataa catgggcaat gacagctctg 960
atcaagaagc ctcaagtact gaacaaagtg caacaagaaa tcagatctgt ggtcggaaag 1020
aaaggcagcg tagccgaaga tgatatacaa aaacttccct attttaaagc ggtggtgaag 1080
gagactetga gaetgtaege accageteca eteteaetge ceagactgae aatcaaaage 1140
agcgtcatag atggatacga cattgaaccc aacaccatag tttacgtgaa cgtttgggcg 1200
attagccgag acaaggattt ttgggagaac ccggatgagt tcttgcccga aagattcttg 1260
aacagtagcg tggactttaa aggccaagat ttcgggtttc ttccattcgg gtcggggcga 1320
agagtgtgcc ctggaatggc cttggggact gcagaagtgg aggtgtcgct tgctaatatt 1380
ctgtattgct tccactggga attgccgcct ggaatggtag aagatgacgt tgatatggac 1440
tttttgcctg gaattactac tcataagaaa aatgcactct atttgatggc caaaagctat 1500
ctg
                                                                  1503
<210> 54
```

<210> 54 <211> 501 <212> PRT <213> Sesamum indicum

<220>

<223> SiP249

<400> 54

Met Ser Ile Pro Leu Leu Ile Ser Leu Ser Leu Ile Ile Leu Val Phe 1 5 10 15

Leu Leu Val Arg Arg Arg Arg Asn Ser Pro Ala Gly Arg Lys Leu Arg
20 25 30

Arg Pro Pro Gly Pro Pro Gly Leu Pro Phe Leu Gly Asn Leu Leu Gln
35 40 45

Tyr Asn Pro Ser Asp Leu His Leu Arg Leu Thr Lys Leu Ser Glu Lys
50 55 60

Tyr Gly Pro Leu Met Tyr Met Thr Phe Val Gly Lys Pro Val Val Val 65 70 75 80

Ile Ser Ser Ala Arg Val Ala Lys Glu Ala Leu Lys Tyr Asn Asp Leu 85 90 95

Ala Phe Ser Ser Arg Pro Ser Thr Ile Ala Ser Arg Lys Val Ala Tyr 100 105 110

Asn Asn Ser Asp Ile Ser Met Ser Pro Tyr Thr Glu Tyr Trp Arg Glu 115 120 125

Leu Arg Lys Met Val Val Leu Arg Leu Phe Thr Val Lys Gln Val Asn 130 135 140

Ser Phe Arg Pro Ala Arg Glu Glu Glu Val Ala Arg Met Val Lys Glu 145 150 155 160

Ile Ser Arg Arg Ala Asn Ala His Gln Pro Val Asn Ile Asn Glu Ile 165 170 175

Ala Leu Ser Leu Ser Ser Arg Met Ile Ser Arg Phe Ala Leu Gly Lys 180 185 190

Arg Tyr Asp Glu Glu Asn Gly Pro Glu Lys Arg Arg Phe Asp Arg Ile 195 200 205

Leu Gln Leu Leu Gln Leu Val Ser Val Glu Ile Phe Phe Gly Asp Tyr 210 215 220

Ser Pro Trp Leu Gly Trp Ile Asp Arg Leu Cys Gly Lys Val Ser Gln 225 230 235 240

Leu Glu Lys Ala Phe Lys Asp Leu Asp Ser Leu Tyr Glu Glu Met Ile 245 250 255

Ala Glu His Leu Ser Pro Asn Arg Pro Glu Ser Met Asn Gly Asp Ile
260 265 270

Leu Asp Met Leu Ile Gln Met Lys Glu Asp Arg Ser Ser Thr Val Gln 275 280 285

Ile Asp Trp Asp His Ile Lys Gly Val Leu Met Asn Met Phe Val Ala 290 295 300

Gly Thr Asp Thr Thr Ala Ala Thr Ile Thr Trp Ala Met Thr Ala Leu 305 310 315 320

Ile Lys Lys Pro Gln Val Leu Asn Lys Val Gln Gln Glu Ile Arg Ser 325 330 335

Val Val Gly Lys Lys Gly Ser Val Ala Glu Asp Asp Ile Gln Lys Leu 340 345 350

Pro Tyr Phe Lys Ala Val Val Lys Glu Thr Leu Arg Leu Tyr Ala Pro 355 360 365

Ala Pro Leu Ser Leu Pro Arg Leu Thr Ile Lys Ser Ser Val Ile Asp 370 375 380

Gly Tyr Asp Ile Glu Pro Asn Thr Ile Val Tyr Val Asn Val Trp Ala 385 390 395 400

Ile Ser Arg Asp Lys Asp Phe Trp Glu Asn Pro Asp Glu Phe Leu Pro
405 410 415

Glu Arg Phe Leu Asn Ser Ser Val Asp Phe Lys Gly Gln Asp Phe Gly
420 425 430

Phe Leu Pro Phe Gly Ser Gly Arg Arg Val Cys Pro Gly Met Ala Leu 435 440 445

Gly Thr Ala Glu Val Glu Val Ser Leu Ala Asn Ile Leu Tyr Cys Phe 450 455 460

His Trp Glu Leu Pro Pro Gly Met Val Glu Asp Asp Val Asp Met Asp 465 470 475 480

Phe Leu Pro Gly Ile Thr Thr His Lys Lys Asn Ala Leu Tyr Leu Met 485 490 495

Ala Lys Ser Tyr Leu 500

<210> 55

<211> 1545

<212> DNA

<213> Sesamum indicum

<220>

<223> SiP288

<400> 55

atggtgggaa ttgtgtatat tgagcttttc ttgtcagtta tgtggtttat ggctttgtgg 60 gtgtggttga attacagggc cctggcgtgg aactggcctg tgatcggaat gctgccgacg 120

cttctgcttc acgtgagccg gattcacgac aattgcacgg agattatggg gaagtcccga 180 cggggaactt ttcatttccg gggtccctgg ttggctgata tggacatgat gggqactqct 240 gatectgaga atgtteacta cattatgage gegaacttee agaattteee gaaaggeeee 300 aagttcaggg aaatttttga tgttcttgga gatgggattt tcaatgcaga ttcggagtcc 360 tggagggacc agagaagggt tgccagggcc ctqatttctc accatggttt cctccqgttt 420 ctggcgaaga tcagccgtga gaaggtagag aaaggcctga ttccagttct tqaaacqqtq 480 tgcctggaaa atcgggtggt cgatttgcag gatttgttcc agaggttgac qtttgataca 540 acttgtacat ttgttactgg ttatgatect ggatgettgt etgttgattt geetgatgtt 600 cctttctcga aagccctaga tgatgccgaa gaagcgatat tcatgcgcca tgtggttcct 660 gaaaagattt ggaaacttca gaggtggttt ggggttggat ctgagagaaa attgagcaaq 720 gctcgtgaag tcttggatag cgtcattggc aggtatatcg cgctgaagcg cggcqaaatq 780 agaagccgag gaatttcgat tgattgtgaa aatgaagatg gtgtggatct gctcacgtct 840 tacatgactg tgggagacga tggtactcaa acccatgatt tgaaatgtga tgacaagttc 900 ttgagggaca cgatactgaa tctaatgatt gcagggcggg acacgacgag ttctgctctg 960 acatggttta tatggcttgt gtcgacacat gctgaagtgg aaaagaggat cagggatgaa 1020 ctgaagtcct ttctgcccgc cggagaacgt gaaaagtggc gtgtgtttgg ggttgaaqaa 1080 accaagaagt tggtttacat gcatggagca atttgcgaag ccctacgact atatccacca 1140 gtcccgttcc agcataagga gccggtggaa ccagatatcc ttccgagcgg gcattttgtg 1200 gaaccgacaa tgaaagtgat gttctcattg tacgccatgg gacggatgga atccgtttgg 1260 ggcgaggatt gcttggaatt caagccggag aggtggattt ctgatagggg atcgatcaag 1320 cacgagecet catacaagtt cttggettte aatgetggte egaggaettg cttggggaag 1380 gatgtggctt tcgctcaggt gaaggcagtg gccgccacct taatccataa ctaccaagtt 1440 cacgtggcag acggccaccg cgtgctgccc aattgttcca tcatcctcta catgaggaat 1500 ggattgaagg ttagggttgc caatagatgg tctgctaaga aaaat <210> 56 <211> 515 <212> PRT <213> Sesamum indicum <220> <223> SiP288 <400> 56 Met Val Gly Ile Val Tyr Ile Glu Leu Phe Leu Ser Val Met Trp Phe 15 Met Ala Leu Trp Val Trp Leu Asn Tyr Arg Ala Leu Ala Trp Asn Trp 25 Pro Val Ile Gly Met Leu Pro Thr Leu Leu Leu His Val Ser Arg Ile 40 His Asp Asn Cys Thr Glu Ile Met Gly Lys Ser Arg Arg Gly Thr Phe 50 His Phe Arg Gly Pro Trp Leu Ala Asp Met Asp Met Gly Thr Ala

Asp Pro Glu Asn Val His Tyr Ile Met Ser Ala Asn Phe Gln Asn Phe

115 120 125

Arg Ala Leu Ile Ser His His Gly Phe Leu Arg Phe Leu Ala Lys Ile 135 Ser Arg Glu Lys Val Glu Lys Gly Leu Ile Pro Val Leu Glu Thr Val 155 Cys Leu Glu Asn Arg Val Val Asp Leu Gln Asp Leu Phe Gln Arg Leu 170 Thr Phe Asp Thr Thr Cys Thr Phe Val Thr Gly Tyr Asp Pro Gly Cys Leu Ser Val Asp Leu Pro Asp Val Pro Phe Ser Lys Ala Leu Asp Asp Ala Glu Glu Ala Ile Phe Met Arg His Val Val Pro Glu Lys Ile Trp Lys Leu Gln Arg Trp Phe Gly Val Gly Ser Glu Arg Lys Leu Ser Lys 225 Ala Arg Glu Val Leu Asp Ser Val Ile Gly Arg Tyr Ile Ala Leu Lys Arg Gly Glu Met Arg Ser Arg Gly Ile Ser Ile Asp Cys Glu Asn Glu 260 Asp Gly Val Asp Leu Leu Thr Ser Tyr Met Thr Val Gly Asp Asp Gly 280 Thr Gln Thr His Asp Leu Lys Cys Asp Asp Lys Phe Leu Arg Asp Thr Ile Leu Asn Leu Met Ile Ala Gly Arg Asp Thr Thr Ser Ser Ala Leu 305 310 Thr Trp Phe Ile Trp Leu Val Ser Thr His Ala Glu Val Glu Lys Arg Ile Arg Asp Glu Leu Lys Ser Phe Leu Pro Ala Gly Glu Arg Glu Lys 345 Trp Arg Val Phe Gly Val Glu Glu Thr Lys Lys Leu Val Tyr Met His Gly Ala Ile Cys Glu Ala Leu Arg Leu Tyr Pro Pro Val Pro Phe Gln 375 His Lys Glu Pro Val Glu Pro Asp Ile Leu Pro Ser Gly His Phe Val 385 390 Glu Pro Thr Met Lys Val Met Phe Ser Leu Tyr Ala Met Gly Arg Met 410 Glu Ser Val Trp Gly Glu Asp Cys Leu Glu Phe Lys Pro Glu Arg Trp

420 425 430

Ile Ser Asp Arg Gly Ser Ile Lys His Glu Pro Ser Tyr Lys Phe Leu 440 Ala Phe Asn Ala Gly Pro Arg Thr Cys Leu Gly Lys Asp Val Ala Phe Ala Gln Val Lys Ala Val Ala Ala Thr Leu Ile His Asn Tyr Gln Val 470 475 His Val Ala Asp Gly His Arg Val Leu Pro Asn Cys Ser Ile Ile Leu 485 Tyr Met Arg Asn Gly Leu Lys Val Arg Val Ala Asn Arg Trp Ser Ala 500 505 Lys Lys Asn 515 <210> 57 <211> 1494 <212> DNA <213> Sesamum indicum <220> <223> SiP168 <400> 57 atggatctac tactttccct tgttctccta ctctgttctg cagcatgcat ttggtttctc 60 cgggtggtcc tgaaacccaa tccagggccc cggaaatcag ccaatctccc tccagggcca 120 aaacctcttc ccataatcgg caacattctt gagcttggtg agaaacccca ccaatctctc 180 gccaaactct ccaaaaccta cgggcccctg atgcgtctca agctgggaac catgacaaca 240 gttgttgtat cctccccgga aatctccagg atcgtgctgc aacaatatga ccaagttttc 300 tccagccgaa cacacgcaga tgccatccga gcacttgacc accacaaaca ttccgtcgcc 360 tggataccgg cggacaatca gtggcggaaa atccgtaaac tgtgcaaaga gaagatgttt 420 tcgggccaaa agcttgatgc gaaccagggc ctgaggaggg agaagttgcg taatttgcaa 480 gactatgtga atgaatgctg cgttagtggc caggtcgtgg atattggtgt agctgccttt 540 acgacgaccc ttaatctgat atcggccact cttttctcgg tggattttgc tgattttggt 600 tctggttcgt ctcaagagct taaggatgtt atgagcggga tagcgtctat catcggccga 660 ccaaattttg ctgattgttt ccctcttctt cggctggttg atccacaggg catcttccgc 720 cagaccacgt tacatttcaa caagtgtttt aagatctttg atgaaattat ccgtcaaagg 780 ctacagacca atgattcggg gacgaaaagt gacatgctga aagagcttct tgaaatcaac 840 cagaaagatg agtctgaatt gagctttgac gagatcaagc atttactcct qqatctactt 900 gtcgcaggaa cggacacaac ttcagttaca gtggaatggg caatgacgga gctagtgcgc 960 caccctgaga aaatgtcgaa agccagaaat gagttaagaa atgtqqtqqq actqaataaa 1020 gaaattcaag aatcagacat ctcaagactc ccttacctac gagcagtggt gaaagaaagt 1080 ttcaggcttc accctgcaac tcctttatcg gtacctcaca aggccgacga ggaagcagaa 1140 atcaatggct atatagtccc taaaggagca caagttctca tgaacgtgtg ggccatcggc 1200 agagattcaa gcatatggag gaaccctgat gtattcatgc ccgagaggtt cttggagaca 1260 gaaattgatg teegtggeea acaettegag etgetteett ttggeggggg gaggaggatt 1320 tgcgtggggc tgccgttagc ctatcgtatg atccatctcg tgcttgccac tttcataagc 1380 gactatgatt ggaaacttga aggagggctg aaaactgaag aaatggacat gagtgaaaag 1440

ttcggcctca ccctgcaaaa agccattcct ctcaaggcac ttccagttaa aatt

```
<210> 58
```

<211> 498

<212> PRT

<213> Sesamum indicum

<220>

<223> SiP168

<400> 58

Met Asp Leu Leu Ser Leu Val Leu Leu Cys Ser Ala Ala Cys
1 5 10 15

Ile Trp Phe Leu Arg Val Val Leu Lys Pro Asn Pro Gly Pro Arg Lys
20 25 30

Ser Ala Asn Leu Pro Pro Gly Pro Lys Pro Leu Pro Ile Ile Gly Asn 35 40 45

Ile Leu Glu Leu Gly Glu Lys Pro His Gln Ser Leu Ala Lys Leu Ser 50 55 60

Lys Thr Tyr Gly Pro Leu Met Arg Leu Lys Leu Gly Thr Met Thr Thr 65 70 75 80

Val Val Ser Ser Pro Glu Ile Ser Arg Ile Val Leu Gln Gln Tyr 85 90 95

Asp Gln Val Phe Ser Ser Arg Thr His Ala Asp Ala Ile Arg Ala Leu 100 105 110

Asp His His Lys His Ser Val Ala Trp Ile Pro Ala Asp Asn Gln Trp
115 120 125

Arg Lys Ile Arg Lys Leu Cys Lys Glu Lys Met Phe Ser Gly Gln Lys 130 135 140

Leu Asp Ala Asn Gln Gly Leu Arg Arg Glu Lys Leu Arg Asn Leu Gln 145 150 155 160

Asp Tyr Val Asn Glu Cys Cys Val Ser Gly Gln Val Val Asp Ile Gly 165 170 175

Val Ala Ala Phe Thr Thr Leu Asn Leu Ile Ser Ala Thr Leu Phe 180 185 190

Ser Val Asp Phe Ala Asp Phe Gly Ser Gly Ser Ser Gln Glu Leu Lys 195 200 205

Asp Val Met Ser Gly Ile Ala Ser Ile Ile Gly Arg Pro Asn Phe Ala 210 215 220

Asp Cys Phe Pro Leu Leu Arg Leu Val Asp Pro Gln Gly Ile Phe Arg 225 230 235 240

Gln Thr Thr Leu His Phe Asn Lys Cys Phe Lys Ile Phe Asp Glu Ile
245 250 250

Ile Arg Gln Arg Leu Gln Thr Asn Asp Ser Gly Thr Lys Ser Asp Met 260 265 270

Leu Lys Glu Leu Leu Glu Ile Asn Gln Lys Asp Glu Ser Glu Leu Ser 275 280 285

Phe Asp Glu Ile Lys His Leu Leu Leu Asp Leu Leu Val Ala Gly Thr 290 295 300

Asp Thr Thr Ser Val Thr Val Glu Trp Ala Met Thr Glu Leu Val Arg 305 310 315 320

His Pro Glu Lys Met Ser Lys Ala Arg Asn Glu Leu Arg Asn Val Val 325 330 335

Gly Leu Asn Lys Glu Ile Gln Glu Ser Asp Ile Ser Arg Leu Pro Tyr 340 345 350

Leu Arg Ala Val Val Lys Glu Ser Phe Arg Leu His Pro Ala Thr Pro 355 360 365

Leu Ser Val Pro His Lys Ala Asp Glu Glu Ala Glu Ile Asn Gly Tyr 370 375 380

Ile Val Pro Lys Gly Ala Gln Val Leu Met Asn Val Trp Ala Ile Gly 385 390 395 400

Arg Asp Ser Ser Ile Trp Arg Asn Pro Asp Val Phe Met Pro Glu Arg 405 410 415

Phe Leu Glu Thr Glu Ile Asp Val Arg Gly Gln His Phe Glu Leu Leu 420 425 430

Pro Phe Gly Gly Arg Arg Ile Cys Val Gly Leu Pro Leu Ala Tyr 435 440 445

Arg Met Ile His Leu Val Leu Ala Thr Phe Ile Ser Asp Tyr Asp Trp 450 455 460

Lys Leu Glu Gly Gly Leu Lys Thr Glu Glu Met Asp Met Ser Glu Lys 465 470 475 480

Phe Gly Leu Thr Leu Gln Lys Ala Ile Pro Leu Lys Ala Leu Pro Val 485 490 495

Lys Ile

<210> 59

<211> 1545

<212> DNA

<213> Sesamum indicum

<220>

<223> SiP236

```
<400> 59
atggcaaacc ccattgattt tctcctcagc ccaacaccat atgtggctac aacccttctt 60
tacqttctct tctctgttct tattgttaga ttcctcagca gaaagctgct cgggaagaag 120
aggtaccatc ccattggtgg taccgtgttc aaccagctgc tgaacttcta taggttqcat 180
gattatatgg ctgatcttgc agggaagtac aagacttaca gactgattgc cccttttcgg 240
actgaggtct atacatctga ccccgctaat gttgagcaca tqttgaaaac qaatttcqaa 300
agttatggca agggacctta caattgcagc attctggggg atttgtttgg tgaaggaatt 360
ttcgcaatcg atggccataa gtggagggag cagagaaaag tgtcaagcct tgagttttct 420
acaagggttc tgagggatta cagtagcatc gtcttcagga aaaacgccgt aaggctcgca 480
aaaattctgt ctggagctgc aacttccaac caaccagtgg atattcaaga tcttttcatg 540
aaatcaactt ttgattctat ttcggaagtt gctttaggag ttgagcttga cagcttgggt 600
ggttcaaatg aagaaggtgc caaatttagc attgctgcag acgacgtgag tatgaggaca 660
ctttggagat acgtggatgt tctgtggaag ttaaagagag ctctaaatgt tggttcagaa 720
gcaaaactga agaaaagcct tcaagtggtt gatgaatttg tgtataagct gattcatagt 780
aggactcagc aaatgaacat gccaggaaat gattctgtta tgcagctgaa gaaagacgac 840
attttgtcaa gattcttgca acttactgag gccactccca agtacttgag ggacataaca 900
ataagcttta tagttgctgg taaagacaca acagcaacaa ctctctcctg gtttatttac 960
atgctttgca agtatcctca tgttcaggaa aaggtggagc aagagataaa agatgcgaca 1020
ggctgcaaag aggtagcaga tatctcagaa ttttcagcct gtgtgacaga agaagctttg 1080
ggcaagatgc attatctcca tgcagcattg acagaaacac tgaggattta tccagcagtt 1140
gcggtggatg caaagcaatg tttgtgtgat gatataatgc cggatgggtt cagtgttaag 1200
aagggggaca tggtggctta tcaaccatat gcaatgggaa ggatgaaatc catatggggt 1260
aatgatgcag aagagttcaa accagagaga tggcttgaca aaaacggttg cttccaqcag 1320
gccagccctt ttaagtttac agctttccag gccggccctc gtctttgttt ggggaaagag 1380
tttgcttatc ggcagatgaa gatattctca gccattctgc tgagattctt taccatgaaa 1440
ctaagtgatg aaagaaagac agtaaactac agaccaatgc tcactcttct catcgacggt 1500
ggtctcattg tccgcccctt tcacagaatg gacgagaaaa ctgca
<210> 60
<211> 515
<212> PRT
<213> Sesamum indicum
<220>
<223> SiP236
<400> 60
Met Ala Asn Pro Ile Asp Phe Leu Leu Ser Pro Thr Pro Tyr Val Ala
Thr Thr Leu Leu Tyr Val Leu Phe Ser Val Leu Ile Val Arg Phe Leu
             2.0
                                                     3.0
Ser Arg Lys Leu Leu Gly Lys Lys Arg Tyr His Pro Ile Gly Gly Thr
Val Phe Asn Gln Leu Leu Asn Phe Tyr Arg Leu His Asp Tyr Met Ala
Asp Leu Ala Gly Lys Tyr Lys Thr Tyr Arg Leu Ile Ala Pro Phe Arg
 65
Thr Glu Val Tyr Thr Ser Asp Pro Ala Asn Val Glu His Met Leu Lys
Thr Asn Phe Glu Ser Tyr Gly Lys Gly Pro Tyr Asn Cys Ser Ile Leu
```

Gly Asp Leu Phe Gly Glu Gly Ile Phe Ala Ile Asp Gly His Lys Trp 115 120 Arg Glu Gln Arg Lys Val Ser Ser Leu Glu Phe Ser Thr Arg Val Leu Arg Asp Tyr Ser Ser Ile Val Phe Arg Lys Asn Ala Val Arg Leu Ala Lys Ile Leu Ser Gly Ala Ala Thr Ser Asn Gln Pro Val Asp Ile Gln Asp Leu Phe Met Lys Ser Thr Phe Asp Ser Ile Ser Glu Val Ala Leu Gly Val Glu Leu Asp Ser Leu Gly Gly Ser Asn Glu Glu Gly Ala Lys 200 Phe Ser Ile Ala Ala Asp Asp Val Ser Met Arg Thr Leu Trp Arg Tyr 210 215 Val Asp Val Leu Trp Lys Leu Lys Arg Ala Leu Asn Val Gly Ser Glu 230 Ala Lys Leu Lys Lys Ser Leu Gln Val Val Asp Glu Phe Val Tyr Lys 245 250 Leu Ile His Ser Arg Thr Gln Gln Met Asn Met Pro Gly Asn Asp Ser Val Met Gln Leu Lys Lys Asp Asp Ile Leu Ser Arg Phe Leu Gln Leu 280 Thr Glu Ala Thr Pro Lys Tyr Leu Arg Asp Ile Thr Ile Ser Phe Ile 290 Val Ala Gly Lys Asp Thr Thr Ala Thr Thr Leu Ser Trp Phe Ile Tyr Met Leu Cys Lys Tyr Pro His Val Gln Glu Lys Val Glu Gln Glu Ile 325 Lys Asp Ala Thr Gly Cys Lys Glu Val Ala Asp Ile Ser Glu Phe Ser Ala Cys Val Thr Glu Glu Ala Leu Gly Lys Met His Tyr Leu His Ala 360 Ala Leu Thr Glu Thr Leu Arg Ile Tyr Pro Ala Val Ala Val Asp Ala 370 Lys Gln Cys Leu Cys Asp Asp Ile Met Pro Asp Gly Phe Ser Val Lys Lys Gly Asp Met Val Ala Tyr Gln Pro Tyr Ala Met Gly Arg Met Lys

				405					410					415		
Ser I	île	Trp	Gly 420	Asn	Asp	Ala	Glu	Glu 425	Phe	Lys	Pro	Glu	Arg 430	Trp	Leu	
Asp L	уys	Asn 435	Gly	Cys	Phe	Gln	Gln 440	Ala	Ser	Pro	Phe	Lys 445	Phe	Thr	Ala	
Phe G	31n 450	Ala	Gly	Pro	Arg	Leu 455	Cys	Leu	Gly	Lys	Glu 460	Phe	Ala	Tyr	Arg	
Gln M 465	let	Lys	Ile	Phe	Ser 470	Ala	Ile	Leu	Leu	Arg 475	Phe	Phe	Thr	Met	Lys 480	
Leu S	Ser	Asp	Glu	Arg 485	Lys	Thr	Val	Asn	Tyr 490	Arg	Pro	Met	Leu	Thr 495	Leu	
Leu I	Ile	Asp	Gly 500	Gly	Leu	Ile	Val	Arg 505	Pro	Phe	His	Arg	Met 510	Asp	Glu	
Lys T	Thr	Ala 515														
<210> 61 <211> 34 <212> DNA <213> Artificial Sequence																
<220> <223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, Bam-SST-FW2																
<400> 61 tggatcccaa ctcatagagt actcaaaaac gctt									34							
<210> 62 <211> 24 <212> DNA <213> Artificial Sequence																
<220> <223>	> De					cific Sec							lly			
-400-		,														

24

<210> 63 <211> 27 <212> DNA <213> Artificial Sequence

gcaaatgatc aaccatggtg ttct

<220>

<400> 63 cacatgaacg agacgaactg ggtttgg

27

<210> 64

<211> 506

<212> PRT

<213> Sesamum radiatum

<220>

<223> SrSiP189

<400> 64

Met Glu Ala Glu Met Leu Tyr Ser Ala Leu Ala Leu Thr Phe Ala Ile 1 5 10 15

Phe Met Val Tyr Arg Ile Leu Ser Asn Ser Gln Glu Lys Ser Ser Leu 20 25 30

Ile Lys Leu Pro Pro Ser Pro Pro Gly Trp Leu Pro Val Ile Gly His
35 40 45

Val His Leu Met Lys Asn Leu Leu His Arg Thr Leu Tyr Asp Phe Ser 50 55 60

Gln Lys Leu Gly Pro Ile Phe Ser Leu Arg Phe Gly Thr Arg Leu Val 65 70 75 80

Val Val Val Ser Ser Ser Ser Leu Val Glu Glu Cys Phe Thr Lys Tyr 85 90 95

Asp Ile Val Leu Ala Asn Arg Pro Gln Pro Ser Val Asp Arg Arg Ser 100 105 110

Leu Gly Phe Ser Thr Thr Ser Val Ile Gly Ala Pro Tyr Gly Asp His 115 120 125

Trp Arg Asn Leu Arg Lys Leu Cys Asp Leu Glu Val Phe Ala Pro Thr 130 135 140

Arg Leu Ala Ser Phe Leu Ser Ile Arg Leu Asp Glu Arg Asp Arg Met 145 150 155 160

Ile Ser Ser Leu Tyr Lys Ile Ser Ser Ala Gly Phe Ala Lys Val Asn 165 170 175

Leu Glu Thr Lys Ile Val Glu Leu Thr Phe Asn Asn Ile Met Arg Met 180 185 190

Val Ala Gly Lys Arg Tyr Tyr Gly Glu Glu Ala Glu Asp Asp Glu Glu
195 200 205

Ala Lys Arg Phe Arg Asp Leu Thr Lys Glu Ala Leu Glu Leu Thr Ser 210 225 220

Ala Ser Asn Pro Gly Glu Ile Phe Pro Ile Leu Arg Trp Leu Gly Phe 225 230 235 240

Asn Gly Leu Glu Lys Lys Leu Ala Val His Ala Arg Lys Thr Asp Glu 245 250 255

Phe Met Gln Gly Leu Leu Asp Glu His Arg Arg Gly Glu Arg Gln Asn 260 265 270

Thr Met Val Asp His Leu Leu Ser Leu Gln Glu Ser Gln Pro Glu Tyr 275 280 285

Tyr Thr Asp Glu Ile Ile Thr Gly Leu Ile Val Ala Leu Ile Ile Ala 290 295 300

Gly Thr Asp Ala Ser Val Val Thr Thr Glu Trp Ala Met Ser Leu Ile 305 310 315 320

Leu Asn His Pro Gln Val Leu Glu Lys Ala Arg Lys Glu Leu Asp Thr 325 330 335

Leu Val Gly His Glu Arg Met Val Asp Glu His Asp Leu Pro Lys Leu 340 345 350

Arg Tyr Leu His Cys Ile Val Leu Glu Thr Leu Arg Leu Phe Pro Ser 355 360 365

Val Pro Thr Leu Val Pro His Glu Pro Ser Glu Asp Cys Lys Ile Gly 370 380

Gly Tyr Asn Val Pro Lys Gly Thr Met Ile Leu Val Asn Ala Trp Ala 385 390 395 400

Ile His Arg Asp Pro Lys Val Trp Asp Asp Pro Leu Ser Phe Lys Pro
405 410 415

Asp Arg Phe Glu Thr Met Glu Val Glu Thr His Lys Leu Leu Pro Phe 420 425 430

Gly Met Gly Arg Arg Ala Cys Pro Gly Ala Gly Leu Ala Gln Lys Phe
435 440 445

Val Gly Leu Ala Leu Gly Ser Leu Ile Gln Cys Phe Glu Trp Glu Arg 450 455 460

Met Ser Ala Glu Lys Ile Asp Leu Asn Glu Gly Ser Gly Ile Thr Leu 465 470 475 480

Pro Lys Ala Lys Thr Leu Glu Ala Met Cys Lys Pro Arg His Ile Met 485 490 495

Glu Arg Val Leu Arg Gln Val Ser Asn Val

```
<210> 65
<211> 1518
<212> DNA
<213> Sesamum radiatum
<220>
<223> SrSiP189
<400> 65
atggaagetg aaatgetata tteagetete geteteacet tegecatatt catggtttae 60
agaattettt etaattegea ggagaaaage ageetgatta agetgeegee gageeegeeg 120
ggttggctcc cggtgatcgg ccacgttcat ctcatgaaaa atctcctcca tagaacacta 180
tacgacttct cccagaaact gggacccata ttttccctcc ggttcggcac ccgcctcgtg 240
gtagtggtgt cctcctcctc cctggtcgag gaatgtttca ccaagtacga cattgtcttg 300
gccaaccgcc ctcagccctc tgtcgaccgg cgctcactcg ggttcagcac caccagcgta 360
ateggegeee egtaegggga eeattggege aacetgegaa agttgtgega tettgaaqta 420
ttcgccccga cccgtctcgc ctcgttttta tccatcaggc ttgacgagag ggaccgcatg 480
atttcgtcgt tgtacaaaat ctcgtccgcc ggtttcgcga aggtgaattt ggagacgaag 540
attgttgagc tgacgtttaa taacataatg aggatggtgg cggggaagag atactatggg 600
gaggaggcgg aggacgacga ggaggcgaag aggttcaggg acctgacgaa ggaggctttg 660
gagttgacga gcgcttccaa tcctggtgag atatttccaa tattgcggtg gcttggtttc 720
aatgggttgg agaagaagct ggctgttcac gcgcggaaga cggatgagtt catgcaaqqq 780
ctgctggacg aacaccgacg gggcgagcgc cagaacacca tggttgatca tttgctttcg 840
ttgcaggaat ctcaacctga gtactacact gatgaaatca tcactggcct catagttgca 900
ttgataattg cgggaacgga tgcatcggtt gtaactacag aatgggcgat gtcccttata 960
ctaaatcatc cccaagtact tgaaaaggct agaaaagaac tggacactct agtaggacac 1020
gaacgcatgg tcgatgaaca tgatctgccc aaactacgtt accttcactg catagtcttg 1080
gagacettaa ggttatttee ttetgtteea aegttggtge cacaegaace ateggaggat 1140
tgtaaaattg ggggatacaa tgtccccaag gggacaatga tactggtgaa tgcttgggca 1200
atacaccgag accccaaggt gtgggacgac cccttgagct ttaagcccga caggtttgag 1260
acaatggaag tggagacaca caagctgttg ccgttcggga tgggcaggag agcgtgtccc 1320
ggagctggat tggcgcagaa gtttgtgggg ttggctttgg ggtcgctgat tcagtgtttc 1380
gagtgggaga gaatgagtgc ggagaaaatt gacttgaacg aaggttctgg gataaccttg 1440
cctaaagcta agacgttgga agccatgtgc aaacctagac atatcatgga gagagttctt 1500
cgtcaggttt cgaacgtc
                                                                   1518
<210> 66
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Artificially
      Synthesized Primer Sequence, NtUBQ-FW
<400> 66
ggaatgcaga tcttcgtcaa
                                                                   20
<210> 67
<211> 18
<212> DNA
<213> Artificial Sequence
```

<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, NtUBQ-RW	
<400> cctaga	67 aaacc accacgga	18
<210><211><212><212><213>	24	
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, SiP189-bam-FW	
<400> ttttca	68 agcca acatggaagc tgaa	24
<210><211><212><213>	24	
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, SiP189-nco-RV	
<400> gcaaa	69 tgatc aaccatggtg ttct	24
<210><211><211><212><213>	25	
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, STAR-LF1	
<400> acgaa	70 gttat gcggccaatt aaccc	25
<210><211><212><212><213>	25	
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, STAR-LR1	

```
<400> 71
ccacctgacg tcgcggccta atacg
                                                                   25
<210> 72
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Artificially
      Synthesized Primer Sequence, M13-47(F)
<400> 72
cgccagggtt ttcccagtca cgac
                                                                   24
<210> 73
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Artificially
      Synthesized Primer Sequence, RV-M(R)
<400> 73
gagcggataa caatttcaca cagg
                                                                   24
<210> 74
<211> 3069
<212> DNA
<213> Sesamun indium
<400> 74
tacgtggttg taaattaagg tggcatagtc aaagctgtgt aggatggagg aattaqacac 60
ttccccagtc ccccacagac tattcccgag ctgaccaaac acagtcgaaa gtgtggggcc 120
caatgaaatt gacagatgac gtctagtgta gtgtgaatgt gtgatatttt tgcagaatat 180
tgtaaaagag ggttcaccaa atctcactag tttgtgacta attgactatt tttgcagaaa 240
attcgtattt agtatagggt cttggtcaaa ttaattaatt atataacaaa tqtqatatat 300
ttaatttgtt attaattttt ttatatttgt tgtgtaatta gttaggattt tatataagaa 360
tttgaaaaaa tgagatgttt ttttgtaaat caaattacac aatatcatgt attgggtttt 420
tegteetgaa gtegettgaa aattgattag ateggeggae ttgaacagae gagtgaatqq 480
acatgattta aaattttaag gataaatata tatagtatca gttatcaaaa taaaaaattt 540
ccttcaaaat catggtcttg tttaagatag ttttttgagt aatgtggcac cataattccc 600
aagcactaga agtgcaattg taaatccaac ggtacctagt ttaattgata aaattaaagt 660
ccaaaaattt tcctgagaaa ccaattcgag caagggtaca tcaaaggtgc caccagggag 720
ttaagcaaga aatgtcccct aaactttagg catgaggtat ccctataaaa taaattgacc 780
taaaaagatt caaatggctt agagtcgaga aaaagactaa gtagaccatt agggaagccc 840
acatgcctaa gatcctccag ccgaagtaga ggcctatgcg gcagtcagcc tagtgacttg 900
ggattcccta gctctgaaag aattaatatt gtcccaagaa tctaaggcta catagtagaa 960
atgaaaacaa agcgaattta aatttgaagc cagcatgatt gaattttttt tttttttt 1020
aggtgtttaa gcactcaaac atgtacaata aataaacgtg tggctaattt aaagaacatt 1080
gaaagctggc caagaattat accttttaaa gcgagtggag tttccgatgt ttqaqctctc 1140
attcaatccg ttcacatcta gatgaacaaa cgtctctttt aatggtatcc acgatacctt 1200
tgtcgagggg atttctcgtc tccttgctag aggattcaat attaccaagg ggtcaaaact 1260
```

```
atactaactt aaagaagatt gagaacacac tattaaattc tcgatcccaa ttttcaagcc 1320
tttgcaccta gttgaaagct tgtgcgtaga gatgcttttg agagagtgtc ggggaggaga 1380
ggggatggaa cacaaaattt taggcttatt ttttcttttt tttttttgtc aaaaatgtct 1440
ctgttaaagt tttgtgcatg tcctctatat gccaaatatt tggtggtaag cacgacaaag 1500
gtatgccaaa tgaagttgta ttaactatgt tgaataagat ggtcctatac taatagatta 1560
cataggccaa cccattagct tgtaggtcac atattccaac ataatgtaga ggtctaagca 1620
caagcagacc catgccatat ggcgtccatg gggtagtcca ggtgatattg acgtaagttc 1680
ttttaagcca catcaacaaa cttcagccgt ccaagcaagg acatgtggcc gcctcaaaag 1740
aaggcctcaa tgcttcctta tccctaaaac aactctagct ttggaaacca gatcagatga 1800
ggatatcccc taagctattt caaaaaatct aggaacctta tctgtagcag actttgttaa 1860
tttttcaaat caagggactc caacagccaa gcgataaccc tcaccaaatt tgtgaaggat 1920
tcgatattat ccaaccagtt gatgatttgc ttataaagtg caatcttccc ccaacaaaaa 1980
agccaattcc aacttttact ttcaaattat agctttaatt tctgacttaa aatttcatat 2040
tataaatttc aatctcttaa gtgtacacaa aatacaagat atttcactct tttgtatttt 2100
totaattocc ataattttat otttattttg tattttgatt gaacccgago acatotttqa 2160
cttgcatcaa caatattagc tctaaattaa acatagaatt taatgttaaa atqaqaaaaq 2220
gaactcatac agatcggact caaaacctta acacctaata aagtatgcat cctaataaaa 2280
agttattacc aaagtgaaat tatgcttaat gaaaatcgaa atcaqaaqta qttcttaatt 2340
ggagagtttc gagacggcaa gaatattgca actcatcctc acacctaccc atctatttca 2400
tactcttaaa ttataatcta attcaatata cacaacaacc tatcacatta atatacaata 2460
tgaaaggtca ataaaatatt tacgctggca aacctcccca gtagaattcg ggcacatatg 2520
aagtgttaac cattcaaata tggacaaagg aacactagag acacgaagtt tatttcaaag 2580
gaaaattttg tctaaaattg aatttaatta aatttaaatt aattatataa taaatataat 2640
gtattttaca tcatgattga tatataattt taaaaaaaaat aattattcca actattaaca 2700
ttaattaata aataactttt acaagaccca ggccaccaac tcccgtccac atgaaagaat 2760
gggtaaccgc taagtctata ttttagtact acgacgtatg caaatacgct ttttccacaa 2820
aaatcaaatt ttaattttta ctttatccaa ggcaagaaaa caaaaaatgc ataaattcac 2880
gttctaattc atcaatactc aagaaatagc atacttgatt tgaactgaga tttgtcactt 2940
tcctacaaat tctgcagact atgaaaacga catcaaccaa ccaatatcca ctctctatat 3000
aaatagcatc acttcactag caatttctca tcaactcata gagtactcaa aaacgctttt 3060
tcagccaac
                                                                  3069
<210> 75
<211> 29
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Artificially
      Synthesized Primer Sequence, gSST-FW1
<400> 75
aatgaaattg acagatgacg tctagtgta
                                                                  29
<210> 76
<211> 30
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Artificially
      Synthesized Primer Sequence, qSST-RV2
<400> 76
ctgcgaatta gaaagaattc tgtaaaccat
                                                                  30
```

<210> 77 <211> 2815 <212> DNA <213> Sesamum radiatum

<400> 77

tagtgtagtg tgaatgtgtg atatttttgc agtatatata ttgtaaaaga ggattaacca 60 aatctctcta gttcgtgatt atgactattt ttgcagaaaa tttgtattta gtttagggtt 120 ggtaaaatct aatttataga gtaaatatga tgtatttatt ttgtgattga ttacttttat 180 atttattgta taattagtta taatttgata aagtgtgata ttttttataa attagattac 240 atattattat gtactgagtt tttcgttctg atgccattta aaaattggtt aggtcgqcqa 300 cttgaactga cgagtgaagg gacttgattt aacattttaa ggatatatat atatagtacc 360 agttatcaaa ataaaagttt totttoaaaa toatagtttt gtttaagata attttgtgag 420 tatatgttgc accacaattc ccaagcacta taagtgcaac tgtaggtcta attggaccta 480 gtttagttga caaaattgaa gtccaagaat atcttcaaga agccaattcg tgtaatggta 540 cgtcaaaggt gccaccaggg aatcaagtag gaaatttccc ctaaatgtta ggcatgaggt 600 gccactataa agaaaattga cccaaagaga tacaagtatc ttagagtcga gaagaagact 660 acgtagacca ttagggaagt ccacatgcct aagattctgc agctgaagca caggcctagg 720 tacggtcagc ccagggactc gagatcccct agctctcaaa gaattggtat tggcccagga 780 atctaaggct acatagcaaa aacgaaaata aaacaaactt aaatttgaag tcaacgggat 840 tgaatcctat tttctcgggt gttcaaactc aagcatgtaa aataaataaa cgtgtgacta 900 atttacaaaa cactgaaaac taattacaaa ttatacctta aaagcatgtq taqtttttaa 960 cgtttgagct ttcgtcaatc cattcacgta gagataaacg gacgtctcct ctaagggtat 1020 ccacaatacc attggcgagg agatttcttg tctattagag gattcgagat taccatggag 1080 ttagaactat aaacctaaag aagatcgaga aaatactatt agattagtgt tctcaatctc 1140 aattctcaag ccttcaaacc tagttaaaag cttgagaaaa tttgtgcgta gatatgtttt 1200 ggagagagtg tcggagagaa gaggggatcg agcacaaact cttagcccta ttctttctc 1260 ttctttgccg aaaaatgtct ttgttagagt ccttgtgcat gttttctata tgccaaatat 1320 gtggtggtaa gcacaacaaa gttatgtgaa aagaaattgt attagcacta cgttgaataa 1380 gattgtcttc tactaataga tgatagaggg caaccattgg cttgtcggtt acttattcca 1440 acataatgta gaggcccaag catgataaga cctatgccac aggacgtcct tgggtggtcc 1500 aagtgatatt gacgtaagac cttttaacct acttcggcag gctttagcca taacctccag 1560 cctgtgaaac ccgatcagat gaggatatcc cctcagcccc tccaaaaatc taggaatctc 1620 atccgcagca gatttcggta tcttttccta gaagatcaaa aaactctaac cactaagaga 1680 taacccccc cacaaaatta atggaaaatt tggccttatc taactggcta ataqqttqcc 1740 cataaattgc gagctccccc aacataaaaa gccaatccaa ctttactttt aaattatagg 1800 tttagtttct aacttaaaat ttcatattat gaatatcaac ctcttatgta tacacaaagt 1860 aacaagatat tttactcatt tgttttctct tagttcctat aattttatct ttcttgcatc 1920 aacaatattt gctctaaatt aaatatagaa tttaatgtta aaatgagaaa acggactcaa 1980 aaccagaaca cctaataaag tatgcatctt aataaaaagt tattacgaag gagaaaaata 2040 tgcttaataa aaatcgaaat cagaagtagt tcttaattgg agagtctgaa aacggcaaga 2100 atattgcaag tcatcctcac tttctcatcc atagacagtc acacctaccc cacatatttc 2160 atacttttaa attattatct aatttaatat acgcatcant tcataatata taatacgaaa 2220 ggttaataaa atatttacgc tagcaaactt cttcagtaga attcatgtac ataagaagtg 2280 ttgaccattc aaatatggaa aaagaaacac tagagataag aaacttagtt gtgaagcaga 2340 aaatatttaa gttggttggt tggatttgaa ctaattaata taataaatat aatatatcgt 2400 gtaaattgaa aaacgactat taacatcaat taataaataa ttttctgtta gtgaagatgg 2460 actacaagac ctaggccacc aacccccatc cacctgaatg aatgggtaac cgctaagtcc 2520 atatttcagt actccggcgt ctgcaaaaac gctttttcca caaaaatcaa attttaagtt 2580 tttactttat cctaggcaag aaaacaaaat atgcatagat tcacgttcaa attcatcaat 2640 gctcaagaaa tagcatactt gatttgaact gagatttgtc actatcctac aaattctqca 2700 cactatgaaa acgacatcaa ccaaccaaaa tccactctct ataaatacca tcacttcact 2760 agcaatttct catcaactca taacgtactc aaataaacac gctttttcag ccaac 2815

<210> 78

<211> 507

<212> PRT

<213> Sesumum alatum

<400> 78

Met Glu Ala Glu Met Leu Tyr Ser Ala Leu Ala Leu Thr Phe Ala Ile 1 5 10 15

Ile Met Val His Arg Ile Leu Ser Asn Ser Gln Asn Lys Arg Ser Leu 20 25 30

Ile Asn Leu Pro Pro Ser Pro Pro Gly Trp Leu Pro Ile Ile Gly His
35 40 45

Leu His Leu Ile Lys Asn Pro Leu His Arg Thr Leu Tyr Asp Cys Ser 50 60

Gln Lys Leu Gly Ser Ile Phe Ser Val Trp Phe Gly Ser Arg Leu Val 65 70 75 80

Val Val Val Ser Ser Ser Leu Val Glu Glu Cys Phe Thr Lys Tyr 85 90 95

Asp Ile Val Leu Ala Asn Arg Pro Asp Leu His Leu Asp Leu Arg Ser 100 105 110

Leu Gly Ala Ser Thr Ile Ser Val Ile Gly Ala Pro Tyr Gly Asp His 115 120 125

Trp Arg Asn Leu Arg Lys Leu Cys Asp Leu Glu Val Phe Ala Pro Thr 130 135 140

Arg Leu Ala Ser Phe Leu Ser Ile Arg Arg Asp Glu Arg Asp Arg Met 145 150 155 160

Ile Ser Gly Leu Tyr Lys Ile Ser Ser Ala Gly Leu Ala Lys Val Asn 165 170 175

Leu Glu Ala Lys Ile Ala Glu Leu Thr Phe Asn Asn Leu Met Arg Met 180 185 190

Leu Ala Gly Lys Ile Tyr Tyr Gly Glu Glu Ala Glu Asp Glu Glu Glu 195 200 205

Ala Lys Arg Phe Arg Asp Met Thr Lys Glu Ala Leu Glu Leu Met Asn 210 215 220

Thr Phe Asn Leu Ala Glu Ile Phe Pro Ile Leu Arg Trp Ile Gly Cys 225 230 235 240

Asn Gly Phe Glu Lys Gln Leu Pro Val His Ser Arg Lys Thr Asp Glu 245 250 255

Ile Met Gln Gly Leu Leu Asp Glu His Arg Arg Gly Glu Arg Gln Asn 260 265 270

Thr Met Val Gly His Leu Leu Ser Leu Gln Glu Ser Gln Pro Asp Tyr 275 280 285 Tyr Thr Asp Glu Ile Ile Thr Gly Leu Ile Ile Ser Leu Ile Ile Ala 295 Gly Thr Asp Ala Ser Val Val Thr Thr Glu Trp Ala Met Ser Leu Leu 310 315 Leu Asn His Pro Lys Val Leu Glu Lys Ala Arg Gln Glu Met Asp Thr 325 330 Leu Val Gly His Glu Arg Met Val Glu Glu Asp Asp Leu Pro Lys Leu 345 Arg Tyr Leu His Tyr Ile Ile Leu Glu Thr Leu Arg Leu Phe Pro Ser 360 Val Pro Thr Leu Val Pro His Glu Pro Ser Glu Asp Cys Asn Ile Gly 370 375 380 Gly Tyr Asn Val Pro Lys Gly Thr Met Ile Ile Val Asn Ala Trp Ala 390 395 Ile His Arg Asp Pro Lys Val Trp Asp Pro Met Ser Phe Lys Pro 410 415 Asp Arg Phe Glu Thr Leu Glu Val Glu Thr His Lys Leu Leu Pro Phe Gly Met Gly Arg Arg Gly Cys Pro Gly Ala Gly Leu Ala Lys Lys Phe 440 Val Gly Leu Ala Leu Ala Ser Leu Ile Gln Cys Phe Asp Trp Glu Arg 450 455 Ile Ser Ala Glu Lys Ile Asp Leu Lys Glu Gly Ala Ser Arg Ile Thr 470 Leu Pro Lys Ala Thr Thr Leu Glu Ala Met Cys Lys Pro Arg His Val 485 490

Met Glu Lys Val Leu Arg Gln Val Ser Asn Val 500 505

<210> 79

<211> 1524

<212> DNA

<213> Sesumum alatum

<400> 79

atggaagctg aaatgctata ttcagctctc gctctcacct tcgccataat catggttcac 60 agaattcttt caaattcaca gaacaagcgc agcctgatca atctgccgcc gagcccgcct 120 ggttggctgc cgattatcgg ccaccttcat ctcataaaaa atccactcca tagaacacta 180 gtggtggtgt cctcctcc cctggtggag gaatgtttca ccaagtacga cattgtcttg 300

gccaaccgcc	ctgacctcca	tctggacctg	cgatcactcg	gggccagcac	catcagcgta	360
atcggggccc	cttacgggga	ccactggcgc	aacctgcgaa	agttgtgcga	tcttgaagta	420
ttcgccccga	cccgtctcgc	ctccttctta	tccatcagac	gagacgagag	ggaccgcatg	480
atttccgggt	tatacaaaat	ctcgtcggcc	ggtttggcga	aggtgaattt	ggaggcgaag	540
attgcggagc	tgacgtttaa	taacttaatg	aggatgttgg	cggggaaaat	atactatggg	600
gaggaggcgg	aggacgagga	ggaggccaag	aggttccggg	acatgacgaa	ggaggctttg	660
gagttgatga	acaccttcaa	tcttgctgag	atatttccga	tattgcggtg	gattgggtgc	720
aatgggttcg	agaagcagct	gcccgttcac	tcgcggaaga	cggatgagat	catgcaaggg	780
ctgctggacg	aacaccgacg	cggcgagcgc	cagaacacca	tggttggtca	tttgctttcc	840
ttgcaggaat	ctcaacctga	ctactacact	gatgaaatca	tcactggcct	cataatttca	900
ttgataatcg	cggggacgga	tgcatccgtt	gtaactacag	aatgggcgat	gtctctttta	960
					ggtaggacat	
gaacgcatgg	tcgaagaaga	cgatctcccc	aaactacgtt	accttcacta	cataatcttg	1080
gagaccttaa	ggttattccc	ttctgttcca	acgttggtgc	cacacgaacc	gtcggaggac	1140
tgtaatattg	ggggatacaa	cgtccccaag	ggcacaatga	tcatcgtgaa	tgcatgggca	1200
atacacagag	accccaaggt	gtgggacgac	cccatgagct	ttaagcccga	caggtttgag	1260
		caagttgttg				1320
ggagctggat	tggcgaagaa	gttcgtggga	ttggctttgg	catcgctgat	ccagtgcttc	1380
gactgggaga	gaattagtgc	cgagaaaatt	gacttgaagg	aaggtgcttc	taggataacc	1440
ttgcctaaag	ctacgacgtt	ggaagccatg				1500
cttcgtcagg	tttcgaacgt	ctga				1524

4675833

SEQUENCE LISTING

<110> SUNTORY LIMITED

<120> A gene encoding an enzyme for catalyzing biosynthesis of lignan, and use thereof

<130> SU0411

<150> JP 2003-341313

<151> 2003-09-30

<150> JP 2003-432383

<151> 2003-12-26

<160> 79

<170> Patentin Ver. 2.1

<210> 1

<211> 506

<212> PRT

<213> Sesamum indicum

<220> <223> SiP189

Met Glu Ala Glu Met Leu Tyr Ser Ala Leu Ala Leu Thr Phe Ala Ile

Phe Met Val Tyr Arg Ile Leu Ser Asn Ser Glin Asp Lys Arg Ser Leu 20 25 30

Thr Lys Leu Pro Pro Ser Pro Pro Gly Trp Leu Pro Val Ile Gly His 35 40

Ala His Leu Met Lys Asn Leu Leu His Arg Thr Leu Tyr Asp Phe Ser 50 60

Gln Lys Leu Gly Pro Ile Phe Ser Ile Arg Phe Gly Ser Arg Leu Val 65 70 75 80

Val Val Val Ser Ser Ser Ser Leu Val Glu Glu Cys Phe Thr Lys Tyr 85 90 95

Asp Ile Val Leu Ala Asn Arg Pro Gln Ala Ser Val Asp Arg Arg Ser 100 105 110

Leu Gly Phe Ser Thr Thr Ser Val Ile Gly Ala Pro Tyr Gly Asp His 115 120 125

Trp Arg Asn Leu Arg Lys Leu Cys Asp Leu Glu Val Phe Ala Pro Thr 130 140

Arg Leu Ala Ser Phe Leu Ser Ile Arg Leu Asp Glu Arg Asp Arg Met 145 150 155 160

Ile Ser Ala Leu Tyr Lys Ile Ser Ser Ala Gly Phe Ala Lys Val Asn 165 170 (175)

Leu Glu Ala Lys Ile Val Glu Leu Thr Phe Asn Asn Ile Met Arg Met 180 185 190

Val Ala Ala Lys Arg Tyr Tyr Gly Glu Glu Ala Glu Asp Asp Glu Glu 195 200 205

Ala Lys Arg Phe Arg Asp Leu Thr Lys Glu Ala Leu Glu Leu Thr Ser 210 220

Ala Ser Asn Pro Gly Glu IIe Phe Pro IIe Leu Arg Trp Leu Gly Cys 225 230 235

Asn Gly Leu Glu Lys Lys Leu Ala Val His Ser Arg Lys Thr Asp Glu 255 of the Asp Clu

Phe Met Gln Gly Leu Leu Asp Glu His Arg Arg Gly Glu Arg Gln Asn 260 265 270

Thr Met Val Asp His Leu Leu Ser Leu Gln Glu Ser Gln PromGlu Tyrmana 285

Tyr Thr Asp Glu Ile Ile Thr Gly Leu Ile Val Ala Leu Ile Ile Ala 290 295

Gly Thr Asp Ala Ser Val Val Thr Thr Glu Trp Ala Met Ser Leu Leu 305 310 315

Leu Asn His Pro Lys: Val Leu Glu Lys Ala? Arg Lys Glu Leu Asp Thro 325 330 335

Leu Val Gly His Glu Arg Met Val Asp Glu His Asp Leu Pro Lys Leu 340 345

Arg Tyr Leu His Cys Ile Val Leu Glu Thr Leu Arg Leu Phe Pro Ser 355 360 365

Val Pro Thr Leu Val Pro His Glu Pro Ser Glu Asp Cys Lys Ile Gly 370 375 380

Gly Tyr Asn Val Pro Lys Gly Thr Met Val Leu Val Asn Ala Trp Ala 385 390 400

lle His Arg Asp Pro Lys Val Tr
p Asp Asp Pro Leu Ser Phe Lys Pro405 $$ 415

Asp Arg Phe Glu Ile Met Glu Val Glu Thr His Lys Leu Leu Pro Phe 420 430

Gly Met Gly Arg Arg Ala Cys Pro Gly Ala Gly Leu Ala Gln Lys Phe 435 440 445

Val Gly Leu Ala Leu Gly Ser Leu Ile Gln Cys Phe Asp Trp Glu Arg 450 460

```
Thr Ser Pro Glu Lys Ile Asp Leu Asn Glu Gly Ser Gly Ile Thr Leu
 Pro Lys Ala Lys Thr Leu Glu Ala Met Cys Lys Pro Arg His Val Met
Glu Lys Val Leu Arg Gln Val Ser Asn Val
 <210> 2
<211> 1518
<212> DNA
 <213> Sesamum indicum
<220>
<223> SiP189
<400> 2
atggaagetg aaatgetata tteagetete geteteacet tegecatatt catggtttae 60
agaattettt etaattegea ggacaagege ageetgaeta agetgeetee gageeegeee 120
ggttggctgc cggtgatcgg ccacgctcat ctcatgaaaa atctcctcca tagaacacta 180
tacgacttet eccagaaact gggaccata ttttccatce ggttegggte gegeetegtg 240
gtggtggtgt cctcctcctc cctggtggag gaatgtttca:ccaagtatga cattgtcttg 300
gcaaatcgcc ctcaggcttc tgttgaccgg cgctcacttg ggttcagcac caccagcgta 360
atcggggccc cgtacgggga ccattggcgc aacctgcgaa agttgtgcga tcttgaagta 420
ttcgccccga cccgtctcgc ctcgttttta tccatcaggc ttgacgagag ggaccgcatg 480 atttcgcgt tatacaaaat ctcgtccgcc ggtttcgcga aggtgaattt ggaagcgaag 540 attgtggagc tgacgtttaa taacataatg aggatggtgg cggcgaagag atactatggg 600 gaggaggcgg aggacgacga ggaggcgaag aggttcaggg acctgacgaa ggaggctttg 660 gagtagggg aggacgacga ggaggcgaag aggttcaggg acctgacgaa ggaggctttg 660
gagttgacga gcgcttccaa tcctggtgag atatttccaa tattgcggtg gcttggttgc 720
aatgggctgg agaagaagct ggctgttcac tcgcggaaga cggatgagtt catgcaaggg 780
ctgctggacg aacaccgacg gggcgagcgc cagaacacca tggttgatca tttgctttcg 840
ttgcaggaat ctcaacctga gtactacact gatgaaatca tcactggcct catagttgca 900
ttgataattg cgggaacgga tgcatcggtt gtaactacag aatgggcgat gtccctttta 960
ctaaatcatc ccaaagtact tgaaaaggct agaaaagaac tggacactct agtaggacac 1020 gaacgcatgg ttgatgaaca cgatctcccc aaactacgtt accttcactg catagtcttg 1080 gagaccttaa ggttattccc ttctgttcca actttggtgc cacacgaacc atcagaggat 1140 tgtaaaattg ggggatacaa tgtccccaag gggacaatgg tattagtgaa tgcttgggca 1200 atacaccgag accccaaggt gtgggacgac cccttgagct ttaagcccga caggtttgag 1260 atacaccgag tgggacaa gaggttgggacgac cccttgagct ttaagcccga caggtttgag 1260
ataatgaag tggagacaca caagttgttg ccgttcggaa tgggcaggag agcgtgtcct 1320 ggagctggac tggcgcagaa gtttgtggg ttggctttgg ggtcgctgat tcagtgtttc 1380 gactgggaga gaacgagtcc cgagaaaatt gacttgaacg aaggttctgg gataaccttg 1440
cctaaagcta agacgttgga agccatgtgc aaacctagac atgtcatgga aaaagttctt 1500
cgtcaggttt ccaacgtt
<210> 3
<211> 21
<212> DNA
<213> Artificial Sequence
```

<400> tatgct	3 ttgtc tcaaagatta: a	21
<210><211><211><212><213>	4 21 DNA Artificial Sequence	
<220>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, Sil8SrRNA-RV	
<400> aacato	•	Ago (1975)
<210> <211>	5	
<212> <213>	DNA Artificial: Sequence sorgal assensorage (a hay agains), blair require - Mil Orango gas graf xeletas, burkset reservant en en el	transfer seemaaan
<2223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence: CYP90A-FW and 120 Augustian	o orgonialista. 1. p. l. – 1. p. 1. 1. p. l. se som in
<400> ttttc	Ode standardino decarditza (2. 1900) ya 1902 kwi 1901 (2. 1903) 55k arrenalio harratza fizi nanozinaka zanzalizka ezanzaliza czatz aagagattyt itgac: 400 / 2002 (2. 1904) ilionaliza (2. 1904) Uko indizionaliza	24: 100: 100: 100: 100: 100: 100: 100: 10
<210><211><211><212>	600 21/1088-22, resussions sexualizate sestimates enumerous 187 outtoether alignmented simplified and testimates of the contraction of the contrac	Harrigeri Harriger Electrophysics
-54132	Artificial Sequence 17321 3774 6 360 38 6 38 6 38 6 38 6 38 6 38 6 38	
	Synthesized Primer Sequence, CYP90A-RV	
tgcca	tctcc aaggsts to the second se	18
<211> <212>	We 7 in the all the setting and the setting and the setting the setting the setting and the setting ~ 24 for the setting and the setting	Contraction of the second
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP72B-FW	
<400> cttaa	tgttc aaatgataat ggat	24
	and the second of the second o	**

<211> <212> <213>		e , e des
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP72B-RV	
<400> gtaaa	8 tcgtt cagggttg	18
<210> <211> <212> <213>	24	
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP71B-FW	
<400> ttcac	g cactg atcateteaa agga	24
<210> <211> <212> <213>	18 all and a suppose rejuling an archive	und () het
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP71B-RV	
<400> agaaa	10 cctgt cagggtta	18
<210> <211> <212> <213>	24	
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP84A-FW	
<400> cttac	ll ccgtg acaatatcaa agca	24
<210> <211> <212> <213>	. 18	
<220>		

<223> .	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP84A-RV	
<400> aaaaac	12 ctcg atggtcta **The state of the state o	18
<210> <211> <212> <213>	13 24	1 + 3 + 4 (2) 4 (5 † 7)
	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP96A-FW	Vall 1917
<400> agtcat	•	24
<210> <211> <212> <213>	14 18.	ત્ર કુકુકુકુકુક સમામ
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP96A-RV	
<400> atccat		٠.
<211> <211> <212>	24	
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP710A-FW	
<400> tccga	agacg aagccatcgg cggt	24
<210> <211> <212> <213>	18	
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP710A-RV	
<400> ctaaa	16 ccggt ccggatcg	18

<210><211><211><212><213>		,. •
<220>		
<400> cgcgt	eggcgc tcaacttcat ccta	24
<210> <211> <212> <213>	18	
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP86A-RV	
<400> atcca	18 tetet etggtttg	18
<211> <212>	19 24 DNA Artificial Sequence	
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP74-FW	
<400> cgaga		24
<210> <211> <212> <213>	18	
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP74-RV	
<400> acgaat		18
<210> <211> <212>	25	

<213>	Artificial Sequence	•	
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP75B-FW		
<400> ttaacg	21 ggata ctgagattaa agcct gwaraelMa meanord to 120 me	25	
<210> <211> <212> <213>	22 18		रहारीक्षक भागवादुर
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP75B-RV	ni Palita	**************************************
<400> aagaa	22 tctct cgggttta - 18 19 19 19 19 11 11 12 12 12 12 13 14 14 14 14 14 14 14 14 14 14 14 14 14	18	.m08%5
<210> <211> <212> <213>	23 24		
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP79F-FW	374 374 374	
<400> gtcac	23 accag acgaaatcaa agct		
<210> <211> <212> <213>	24 18		
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP79F-RV	·	:
<400> aggtg	acgct ccggtttg	18	
<210> <211> <212> <213>	~ 24		
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP81D-FW	-	

<400> tacate	25 ggacc gcatcatcaa agga seetypii insee	24.
<210> <211> <212> <213>		
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP81D-RV	
<400> tcgaad	26 cctct ctggcttg	18
<211><212>	27 24 DNA Artificial Sequence	
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP705A-FW	
<400> catato	27 caagt cgcttctcac ggta	24
<210> <211> <212> <213>	28 18	
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP705A-RV	
<400> agaaa	28 cctct ctggttta	18
<210> <211> <212> <213>	24	
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, CYP83A-FW	
<400> tttac	29 tgatg ataatgtcaa agcc	24

<210> <211> <212> <213>	18	1、克莱克·维纳人公司 概念	to the Application of the Applic
<220> <223>	Description of Artificial Sequence: Artific Synthesized Primer Sequence, CYP83A-RV	cially	
<400> agaaac	30 ctct cgggccta 《音····································		10
<210> <211> <212> <213>	21		as wright,
<220> <223>	Description of Artificial Sequence: Artificial Synthesized Primer Sequence, SiP168-FW	cially managed respit	タ、2007 2007 2007 2007 2007 2007 2007 2007
<400> tttccc	ettgt tetectaete t		21
<210> <211> <212> <213>	32 21	Proportings of the party The State of State of the State of the State of State of State of the S	
<220> <223>	Description of Artificial Sequence: Artifi Synthesized Primer Sequence, SiP168-RV	cially	er voger Egyptischer Without State
<400> aaata	32 atgat agctaaattt t		21
<210> <211> <212> <213>	21		
<220> <223>	Description of Artificial Sequence: Artifi Synthesized Primer Sequence, SiP189-FW	cially	
<400> tcgtt	.33 tttat ccatcagget t		21
<210><211><211><212><213>	21 DNA		

<220 <223	> > Description of Artificial Sequence: Artificially Synthesized Primer Sequence, SiP189-RV	
<400) caaac	> 34 cgttgg aaacctgacg a	21
	> 35	
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, SiP236-FW	
<400> ggatg	35 Ettctg tggaagttaa a	21
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, SiP236-RV	•
<400> atcta	36 agttt catgcagttt t	21
<210> <211> <212> <213>	37 21 DNA Artificial Sequence	
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, SiP249-FW	
(400> taag	37 cttca aaatgtcgat a	21
(210> (211> (212> (213>	. 21	
(220> (223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, SiP249-RV	
400>	38	

ccaact	Tact tattacagat a $(4\hat{g})^{2\hat{G}}(x)$, i.e. $(p_{\hat{G}}(x)^{\hat{G}$	Sand Agent San George	Z1
<210> <211> <212> <213>	39 21	n in werd in growing in in it. In in a specific section in the	
<220> <223>	Description of Artificial Sequence: Artificial Synthesized Primer Sequence, SiP288-FW	ially Samon Islan	300 T
<400> aaaats	ggtgg gaattgtgta t	Maria de la Santa de la constanta de la consta	21 % (6.3)
<210> <211> <212> <213>	19	anasianasya	1 %1
<220> <223>	Description of Artificial Sequence: Artific Synthesized Primer Sequence, SiP288-RV	-	7. (%) 1. (%) 2. (%)
<400> tacat	40 ctcaa ttttctta 大约、克克克尔斯 A Senement 引力的行	eminan adalah Tertukan berahan Tertukan	19
<210> <211> <212> <213>	41 32		- 18 00kg
<220> <223>	Description of Artificial Sequence: Artifi Synthesized Primer Sequence, GR-SiP168-RV	cially	
<400> cacga	41 tects gagatttees gggaggatae aa		32
<210> <211> <212> <213>	42 18	`st	· · · · · · · · · · · · · · · · · · ·
<220> <223>	Description of Artificial Sequence: Artific Synthesized Primer Sequence, GR-SiP168-Nest	ially . -RV	
<400> gtage	ttttg gagagttt		18
<210>	43		-

yi '-

<212> <213>	DNA Artificial Sequence	
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, GR-SiP189-RV	
<400> ctcgt	43 cgtcc tccgcctcct ccccatagta t	31
<210> <211> <212> <213>	$\overline{21}$	
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, GR-SiP189-Nest-RV	
<400> accate	44 cctca ttatgttatt a	21
<210> <211> <212> <213>	28	
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, GR-SiP236-RV	
<400> ccagga	45 agaga gttgttgctg ttgtgtct	28
<210> <211> <212> <213>	18	
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, GR-SiP236-Nest-RV	
<400> tataaa	46 agctt attgttat	18
(210> (211> (212> (213>	33	
(220>	Description of Artificial Sequence: Artificially	

· 2M	ithesized Primer Sequence, SiP168-BamHI-FW		4.	*
<400> 47		este est però e la companya. La	·	
ggatccaaa	a gagcaaatta tggatctact act		33	11.
1	at attitud to an anagender	many dia and a		.i.
<210> 48 <211> 33				
<212> DNA	V Alagra a	rina di salaja mataga.		
<213> Art	tificial Sequence			
<220>				. 1 ; 11 ,
<223> Des	scription of Artificial Sequence: Artificia	ally	:	1
Syl	nthesized Primer Sequence, SiP168-Xhol-RV	onoupod (sioi)	A Property	
<400> 48		emograe, transt		
ctcgagaag	gg gaaaataatg atagctaaat ttt xiligidshid Moonaagaad (2000)	to a transfer of the second	33	
	Angrence, file-S11186-Nesd-ht	estree Primer	diane.	
<210> 49 <211> 30				e e e
<212> DNA		a. Haddwinia	, <i>I</i> ,	
<213> Ar	tificial Sequence			
<220>			· Offi	
<223> Des	scription of Artificial Sequence: Artificia nthesized Primer Sequence, SiP189-BamH1-FW	lly .	, je	
ု သွား		e deseppe in the style		
<400> 49	tt cagccaacat ggaagctgaa			A B F
ggallell	Anthriba MinA Loonoppoli Exilian	11 8 149 1 6 01 160	Yarisa C	
<210> 50	19 78 93 2 AT ARRIVED	many of horizing	df my	
<211> 33				
<212> DN		1 .1 .1.		
<213> Ar	tificial Sequence			
<220>		. 1.5		
	scription of Artificial Sequence: Artifici nthesized Primer Sequence, SiP189-Xhol-RV	ally	,	
		to the second of		
<400> 50 ctcgagaa	aa agagcatcat ttaatcatac act		33	•
	The control of the co	Same of the state		
<210> 51	in the start of the second of	- 19	: ' ,	
<211> 35	•			٠,
<212> DN <213> Ar	A tificial Sequence	4.3		•:•:.
<220> <223> De	scription of Artificial Sequence: Artificia	Hv		
Sy	nthesized Primer Sequence, SiP236-BamHI-FW	· · · · J		
<400> 51				
	ca cttcacttca ttgctcaatg gcaaa		. 35	

```
<210> 52
  <211> 33
  <212> DNA The rest of the first state of the rest o
  <213> Artificial Sequence
  Synthesized Primer Sequence, SiP236-Xhol-RV
  <400> 52
  ctcgagaaca gctgagaccc cacagcaatc taa
                                                                                                                                                                                         33
  <210> 53
 <211> 1503
<212> DNA
  <213> Sesamum indicum
 <220>
<223> SiP249
                                              The state of the state of the state of the state of
 <400> 53
 atgtcgatac ctctccttat ctctctcta ttaatcatcc ttgttttcct actagtccga 60 cgacgccgca acagcccggc tggtcgaaaa ctccggcgtc ctccgggcc tcctggcctt 120 cccttcctcg ggaacttgct ccaatacaac ccctccgatc tccatctccg cctgacaaaa 180
 ctctcagaaa agtacggccc gcttatgtac atgacgttcg tcggaaagcc cgtggttgtg 240 atttcatcgg cccgagtggc caaagaggct ttgaagtaca atgaccttgc attttcgagc 300 aggccttcta ccattgcatc gcgcaaagtg gcttacaaca acagtgacat ctccatgtca 360
ccgtacacag agtactgag agaactgcgg aaaatggtcg ttcttcgct ctttacggtc 420 aaacaagtga actcttccg ccctgctcga gaagaagaag tggcccgcat ggtgaaagag 480 atttccagac ggsccaacgc gcatcagcc gttaacatta atgaaatagc gttgtcgttg 540
 tcgagcagga tgatatctag gtttgcactg gggaagaggt acgacgagga gaacgggccg 600 gaaaagagga ggttcgacag gattctgcag ctgcttcagt tggtgtcggt ggaaattttc 660
 tttggtgatt attctccatg gctgggctgg attgacagac tgtgtggtaa ggtttctcag 720
 cttgagaagg cgttcaagga tttggattca ttgtatgaag agatgatcgc ggagcatctg 780
agcccgaata ggcccgagtc tatgaacgga gacattcttg atatgctaat tcagatgaaa 840 gaagatcggt cgtcgacggt tcaaattgat tgggatcata tcaagggcgt actcatgaac 900
atgiticgtag ccggaacaga cacaactgca gctacaataa catgggcaat gacagctctg 960
atcaagaagc ctcaagtact gaacaaggt caacaagaaa tcagatctgt ggtcggaaag 1020
aaaggcagcg tagccgaaga tgatatacaa aaacttccct attttaaagc ggtggtgaag 1080
gagactetga gactgtacge accageteca eteteactge ceagactgae aatcaaaage 1140
agcgtcatag atggatacga cattgaaccc aacaccatag tttacgtgaa cgtttgggcg 1200 attagccgag acaaggattt ttgggagaac ccggatgagt tcttgcccga aagattcttg 1260 aacagtagcg tggactttaa aggccaagat ttcgggtttc ttccattcgg gtcggggcga 1320
agaststscc ctssaatssc cttssssact scasaastss agststcsct tsctaatatt 1380
ctgtattgct tccactggga attgccgcct ggaatggtag aagatgacgt tgatatggac 1440
tttttgcctg gaattactac tcataagaaa aatgcactct atttgatggc caaaagctat 1500
ctg
<210> 54
<211> 501
<212> PRT
<213> Sesamum indicum
```

<220>

and application

<223> SiP249

<400> 54 is the $15\,\mathrm{ms}$.

Leu Leu Val Arg Arg Arg Arg Asn Ser Pro Ala Gly Arg Lys Leu Arg A first probability of 25 symmetric for a section $30\,$ stables and $12.27\,$

13 Jan X 19854 C. Britishaws State of School School Arg Pro Pro Gly Pro Pro Gly Leu Pro Phe Leu Gly Asn Leu Leu Gln

ng karama antipaggan recapitals to Tyr Asn Pro Ser Asp Leu His Leu Arg Leu Thr Lys Leu Ser Glu Lys 50 60

Tyr Gly Pro Leu Met Tyr Met Thr Phe Val Gly Lys Pro Val Val 65 70 75 80 90 Jakes

CHESCALL TO HEROBY, OF Ile Ser Ser Ala Arg Val Ala Lys Glu Ala Leu Lys Tyr Asn Asp Leu 85 90 95

Ala Phe Ser Ser Arg Pro Ser Thr Ile Ala Ser Arg Lys Val Ala Tyr 105

Asn Asn Ser Aspalle: Ser Meto Ser Pro Tyro Thro Glua Tyro Trp Arg Glua composition of the series of

Leu Arg Lys Met Val Val Leu Arg Leu Phe Thr Val Lys Gln Val Asn

130 Ser Phe ArgaPro Ala Arg Glu Glu Val Ala Arg Met Val Lys Glus and ArgaPro 160 Services and Ar

145

Ile Ser Arg Ala Asn Ala His Gln Pro Val Asn Ile Asn Glu Ile
165

Ala Leu Ser Leu Ser Ser Arg Met Ile Ser Arg Phe Ala Leu Gly Lys

Arg Tyr AspaGlu Glu Asn Gly Pro Glu Lys Arg Arg Phe Asp Arg He 205

Leu Gln Leu Leu Gln Leu Val Ser Val Glu IIe Phe Phe Gly Asp Tyr $210\,$ M , and all compares train 215 , from the regions $a_{
m co}=220\,$ as given by the compares $a_{
m co}$

Martin Administration of the Control Ser Pro Trp Leu Gly Trp Ile Asp Arg Leu Cys Gly Lys Val Ser Gln 235 235 240

Leu Glu Lys Ala Phe Lys Asp Leu Asp Ser Leu Tyr Glu Glu Met IIe 245 250 255

Ala Glu His Leu Ser Pro Asn Arg Pro Glu Ser Met Asn Gly Asp Ile 260 265 270

Leu Asp Met Leu Ile Gln Met Lys Glu Asp Arg Ser Ser Thr Val Gln 275 280 285

Ile Asp Trp Asp His Ile Lys Gly Val Leu Met Asn Met Phe Val Ala Gly Thr Asp Thr Thr Ala Ala Thr Ile Thr Trp Ala Met Thr Ala Leu 305

lle Lys Lys Pro Gln Val Leu Asn Lys Val Gln Gln Glu lle Arg Ser 325 330 335

Val Val Gly Lys Lys Gly Ser Val Ala Glu Asp Asp Ile Gln Lys Leu 345

Pro Tyr Phe Lys Ala Val Val Lys Glu Thr Leu Arg Leu Tyr Ala Pro 355 360 365

Ala Pro Leu Ser Leu Pro Arg Leu Thr Ile Lys Ser Ser Val Ile Asp 370 380

Gly Tyr Asp Ile Glu Pro Asn Thr Ile Val Tyr Val Asn Val Trp Ala 385 390 395 400

lle Ser Arg Asp Lys Asp Phe Trp Glu Asn Pro Asp Glu Phe Leu Pro 405 415

Glu Arg Phe Leu Asn Ser Ser Val Asp Phe Lys Gly Gln Asp Phe Gly 420 425 430

Phe Leu Pro Phe Gly Ser Gly Arg Arg Val Cys Pro Gly Met Ala Leu 435

Gly Thr Ala Glu Val Glu Val Ser Leu Ala Asn Ile Leu Tyr Cys Phe 450 455 460

His Trp Glu Leu Pro Pro Gly Met Val Glu Asp Asp Val Asp Met Asp 465 470 475 480

Phe Leu Pro Gly Ile Thr Thr His Lys Lys Asn Ala Leu Tyr Leu Met 485 490 495

Ala Lys Ser Tyr Leu 500

<210> 55

<211> 1545 <212> DNA

<213> Sesamum indicum

<220>

<223> SiP288

<400> 55
atggtgggaa ttgtgtatat tgagcttttc ttgtcagtta tgtggtttat ggctttgtgg 60
gtgtggttga attacaggc cctggcgtgg aactggcctg tgatcggaat gctgccgacg 120
cttctgcttc acgtgagccg gattcacgac aattgcacgg agattatggg gaagtcccga 180
cggggaactt ttcatttccg gggtccctgg ttggctgata tggacatgat ggggactgct 240
gatcctgaga atgttcacta cattatgagc gcgaacttcc agaatttccc gaaaggcccc 300

```
18/35
aagttcaggg aaattttga tgttcttgga gatggattt tcaatgcaga ttcggagtcc 360 tggagggacc agagaaggst tgccagggc ctgatttctc accatgstt cctccgstt 420 ctggcgaaga tcagccgtga gaaggtagag aaaggcctga ttccagttct tgaaacggtg 480 tgcctggaaa atcgggtggt cgatttgcag gatttgtcc agaggttgac gtttgataca 540 acttgtacat ttgttactgg ttatgatcct ggatgcttgt ctgttgattt gcctgatgtt 600 cctttctcga aagccctaga tgatgccgaa gaagggatat tcatgcgcca tgtggttcct 660 gaaaggttt ggaaacttca gaggtggttt ggggttggat ctgaggaaa attgagcaag 720 gctcgtgaag tcttggatag cgtcattggc aggtatatcg cgctgaagcg cggcgaaatg 780 agaaggcgag gaatttcgat tgatgtgaa aatgagatg gtgggatct gctcacgtct 840 tacatgactg tgggagacga tggtactcaa acccatgatt tgaaatgtga tgacaagttc 900 ttgagggaca cgatactgaa tctaatgatt gcagggcgg acacgacgag ttctgctctg 960 acatggtta tatggcttgt gtcgacacat gctgaagtgg aaaagaggat cagggatgaa 1020 ctgaagtcct ttctgcccgc cggagaacgt gaaaagtggc gtgtgtttgg ggttgaagaa 1080 accaagaagt tggttacat gcatggagaa ccagatgaa ccagataga gccgttcgaagt gtctcattg 1200 gaaccgacaa tgaaagtgat gttctcattg tacgccatgg gacggatgga atccgtttgg 1260 ggcgaggatt gcttggaatt caaggcgga aggtggattt ctgataggg atcgatcaag 1320 ggcgaggatt gcttggaatt caaggcgga aggtggattt ctgataggg atcgatcaag 1320
       aagttcaggg aaatttttga tgttcttgga gatgggattt tcaatgcaga ttcggagtcc 360
        ggcgaggatt gcttggaatt caagccggag aggtggattt ctgatagggg atcgatcaag 1320 cacgagcctt catacaagtt cttggctttc aatgctggtc cgaggacttg cttggggaag 1380 gatgtggctt tcgctcaggt gaaggcagtg gccgccacct taatccataa ctaccaagtt21440 cacgtggcag acggccaccg cgtgctgccc aattgttcca tcatcctcta catgaggaat 1500
            ggattgaagg ttagggttgc caatagatgg tctgctaaga aaaat 1545
                 <210> 56
                                                                                                                                                                                                   The state of the first war are the delication of the state of the first state of the state of th
                 <211> 515
                 <212> PRT
              <213> Sesamum indicum
<2000</p>
<a href="https://doi.org/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007/ph/10.1007
              <220> SiP288

2010 FG

2010 FG
```

Met Val Gly He Val Tyr He Glu Leu Phe Leu Ser Val Met Trp Phe

Met Ala Leu Trp Val Trp Leu Asn Tyr Arg Ala Leu Ala Trp Asn Trp 20 25 30

Pro Val Ile Gly Met Leu Pro Thr Leu Leu Leu His Val Ser Arg Ile 35 40 45

His Asp Asn Cys Thr Glu Ile Met Gly Lys Ser Arg Arg Gly Thr Phe 50 60

His Phe Arg Gly Pro Trp Leu Ala Asp Met Asp Met Met Gly Thr Ala 65 70 75 80

Asp Pro Glu Asn Val His Tyr Ile Met Ser Ala Asn Phe Gln Asn Phe 85 90 95

Pro Lys Gly Pro Lys Phe Arg Glu Ile Phe Asp Val Leu Gly Asp Gly 100 105 110

lle Phe Asn Ala Asp Ser Glu Ser Trp Arg Asp Gln Arg Arg Val Ala 115 120 125

Arg Ala Leu Ile Ser His His Gly Phe Leu Arg Phe Leu Ala Lys Ile

130 135 140 Ser Arg Glu Lys Val Glu Lys Gly Leu Ile Pro Val Leu Glu Thr Val Cys Leu Glu Asn Arg Val Val Asp Leu Gln Asp Leu Phe Gln Arg Leu 165 170 175 Thr Phe Asp Thr Thr Cys Thr Phe Val Thr Gly Tyr Asp Pro Gly Cys 180 185 190 Leu Ser Val Asp Leu Pro Asp Val Pro Phe Ser Lys Ala Leu Asp Asp 195 200 205 Ala Glu Glu Ala Ile Phe Met Arg His Val Val Pro Glu Lys Ile Trp 210 215 220 Lys Leu Gln Arg Trp Phe Gly Val Gly Ser Glu Arg Lys Leu Ser Lys 225 230 235 240 Ala Arg Glu Val Leu Asp Ser Val Ile Gly Arg Tyr Ile Ala Leu Lys 245 250 255 Arg Gly Glu Met Arg Ser Arg Gly Ile Ser Ile Asp Cys Glu Asn Glu 260 265 270 Asp Gly Val Asp Leu Leu Thr Ser Tyr Met Thr Val Gly Asp Asp Gly 275 Thr Gln Thr His Asp Leu Lys Cys Asp Asp Lys Phe Leu Arg Asp Thr 290 295 300 lle Leu Asn Leu Met Ile Ala Gly Arg Asp Thr Thr Ser Ser Ala Leu 305 310 315 320 Thr Trp Phe Ile Trp Leu Val Ser Thr His Ala Glu Val Glu Lys Arg 325 330 335 lle Arg Asp Glu Leu Lys Ser Phe Leu Pro Ala Gly Glu Arg Glu Lys 340 345 350 Trp Arg Val Phe Gly Val Glu Glu Thr Lys Lys Leu Val Tyr Met His 355 360 365 Gly Ala Ile Cys Glu Ala Leu Arg Leu Tyr Pro Pro Val Pro Phe Gln 370 380 His Lys Glu Pro Val Glu Pro Asp Ile Leu Pro Ser Gly His Phe Val Glu Pro Thr Met Lys Val Met Phe Ser Leu Tyr Ala Met Gly Arg Met 405 410 415 Glu Ser Val Trp Gly Glu Asp Cys Leu Glu Phe Lys Pro Glu Arg Trp 420 425 430 lle Ser Asp Arg Gly Ser Ile Lys His Glu Pro Ser Tyr Lys Phe Leu

435 440 445

Ala Phe Asn Ala Gly Pro Arg Thr Cys Leu Gly Lys Asp Val Ala Phe 450 455

Ala Gln Val Lys Ala Val Ala Ala Thr. Leu Ile His Asn Tyr Gln Val 465 470 480

His Val Ala Asp Gly His Arg Vale Leu Pro Asn Cys Ser IIe IIe Leu 485 (H) 490 (200)

Tyr Met Arg Asn Gly Leu Lys Val Arg Val Ala Asn Arg Trp Ser Ala

Lys Lys Asn and and and and and level bed to be seen and row and the second and and the second a

The second of the seco

<211> 1494

<212> DNA continued at Actally confirmed and a transfer of the confirmed and an entire confirmed an

<210> 58 <211> 498

<212> PRT

<213> Sesamum indicum

<220> <223> SiP168

<400> 58
Met Asp Leu Leu Leu Ser Leu Val Leu Leu Leu Cys Ser Ala Ala Cys
1 5 10 15

lle Trp Phe Leu Arg Val Val Leu Lys Pro Asn Pro Gly Pro Arg Lys 25. 30

Ser Ala Asn Leu Pro Pro Gly Pro Lys Pro Leu Pro Ile Ile Gly Asn 35 40 45

lle Leu Glu Leu Gly Glu Lys Pro His Gln Ser Leu Ala Lys Leu Ser 50 60.

Lys Thr Tyr Gly Pro Leu Met Arg Leu Lys Leu Gly Thr Met Thr Thr 65 70 75 80

Val Val Val Ser Ser Pro Glu IIe Ser Arg IIe Val Leu Gln Gln Tyr 85 90 95

Asp Gln Val Phe Ser Ser Arg Thr His Ala Asp Ala Ile Arg Ala Leu 100 105 110

Asp His His Lys His Ser Val Ala Trp Ile Pro Ala Asp Asn Gln Trp 115 120 125

Arg Lys Ile Arg Lys Leu Cys Lys Glu Lys Met Phe Ser Gly Gln Lys 130 135 140

Leu Asp Ala Asn Gln Gly Leu Arg Arg Glu Lys Leu Arg Asn Leu Gln 145 150 155 160

Asp Tyr Val Asn Glu Cys Cys Val Ser Gly Gln Val Val Asp Ile Gly 165 175

Val Ala Ala Phe Thr Thr Thr Leu Asn Leu Ile Ser Ala Thr Leu Phe 180 185 190

Ser Val Asp Phe Ala Asp Phe Gly Ser Gly Ser Ser Gln Glu Leu Lys 195 200 205

Asp Val Met Ser Gly Ile Ala Ser Ile Ile Gly Arg Pro Asn Phe Ala 210 220 .

Asp Cys Phe Pro Leu Leu Arg Leu Val Asp Pro Gln Gly Ile Phe Arg 225 235 230 240

Gln Thr Thr Leu His Phe Asn Lys Cys Phe Lys Ile Phe Asp Glu Ile 245 250 255

lle Arg Gln Arg Leu Gln Thr Asn Asp Ser Gly Thr Lys Ser Asp Met 265 270

Leu Lys Glu Leu Leu Glu IIe Asn Gln Lys Asp Glu Ser Glu Leu Ser

Phe Asp Glu IIe Lys His Leu Leu Leu Asp Leu Leu Val Ala Gly Thr.... 290

Asp Thr Thr Ser Vall Thr Val Glu Trp Ala Met Thr Glu Leu Val Arg 305 310 315

Gly Leu Asn Lys Glu IIe Gln Glu Ser Asp IIe Ser Arg Leu Pro Tyr, 340 345 350

Leu Arg Ala Val Val Lys Glu Ser, Phe Arg Leu His Pro Ala Thr Pro 355 360 365

Leu Ser Val Pro His Lyst Ala Asp Glu Glu Ala Glu IIe Asp Gly Tyr, 375

Ile Val Pro Lys Glý Ala Gln Val Leu Met Asn Val Trp Ala Ile Gly 400 385 395 400

Arg Asp Ser Ser He Trp Arg Asp Pro Asp Val Phe Met Pro Glu Arg 415

Phe Leu Glu Thr Glu He Asp Val Arg Gly Gln His Phe Glu Leu Leu 420 425 430

Pro Phe Gly Gly Arg Arg Ide Cys Val Gly Leu Pro Leu Ala Tyr 435

Arg Met IIe His Leu Val Leu Ala Thr Phe IIe Ser Asp Tyr Asp Trp 450

Lys Leu Glu Gly Gly Leu Lys Thr Glu Glu Met Asp Met Ser Glu Lys 465 470 475 480

Phe Gly Leu Thr Leu Gln Lys Ala Ile Pro Leu Lys Ala Leu Pro Val ... 485

Lys Ile

<210> 59

<211> 1545

<212> DNA <213> Sesamum indicum

22205

<223> SiP236

<400> 59

atggcaaacc ccattgattt tctcctcagc ccaacaccat atgtggctac aacccttctt 60 tacgttctct tctctgttct tattgttaga ttcctcagca gaaagctgct cgggaagaag 120

```
aggtaccatc ccattggtgg taccgtgttc aaccagctgc tgaacttcta taggttgcat 180
  gattatatgg ctgatcttgc agggaagtac aagacttaca gactgattgc cccttttcgg 240
 actgaggtct atacatctga ccccgctaat gttgagcaca tgttgaaaac gaatttcgaa 300 agttatggca agggacctta caattgcagc attctggggg atttgtttgg tgaaggaatt 360 ttcgcaatcg atggccataa gtggagggag cagagaaaag tgtcaagcct tgagttttct 420 acaagggttc tgagggatta cagtagcatc gtcttcagga aaaacgccgt aaggctcgca 480
aaaattetgt etgagetge aactteeaac caaceagtgg atatteaaga tettteatg 540 aaateaactt ttgattetat tteggaagtt getttaggag ttgagettga eagettgggt 600 ggtteaaatg aagaaggtge caaatttage attgetgeag aegaegtgag tatgaggaea 660 etttggagat aegtggatgt tetgtggaag ttaaagagag etetaaatgt tggtteagaa 720 geaaaactga agaaaageet teaagtggtt gatgaatttg tgtataaget gatteatagt 780
 aggactcagc aaatgaacat gccaggaaat gattctgtta tgcagctgaa gaaagacgac 840
 attitgtcaa gattettgca acttactgag gccactccca agtacttgag ggacataaca 900
 ataagettta tagttgetgg taaagacaca acageaacaa eteteteetg gtttatttae 960 atgetttgea agtateetea tgtteaggaa aaggtggage aagagataaa agatgegaca 1020
 ggctgcaaag aggtagcaga tatctcagaa ttttcagcct gtgtgacaga agaagctttg 1080
ggcaagatgc attatctcca tgcagcattg acagaaacac tgaggattta tccagcagtt 1140 gcggtggatg caaagcaatg tttgtgtgat gatataatgc cggatgggtt cagtgttaag 1200
 aagggggaca tggtggctta tcaaccatat gcaatgggaa ggatgaaatc catatggggt 1260
 aatgatgcag aagagttcaa accagagaga tggcttgaca aaaacggttg cttccagcag 1320
gccagcctt ttaagtttaa agctttcag gccggcctc gtcttgttt ggggaaagag 1380 tttgcttatc ggcagatgaa gatattctca gccattctgc tgagattctt taccatgaaa 1440 ctaagtgatg aaagaaagac agtaaactac agaccaatgc tcactcttct catcgacggt 1500 ggtctcattg tccgccctt tcacagaatg gacgagaaaa ctgca 1545
                                                    and the second of the second o
```

<210> 60 <211> 515 <212> PRT

<213> Sesamum indicum

<220> <223> SiP236

<400> 60 Met Ala Asn Pro IIe Asp Phe Leu Leu Ser Pro Thr Pro Tyr Val Ala 10 15

Thr Thr Leu Leu Tyr Val Leu Phe Ser Val Leu IIe Val Arg Phe Leu 20 25 30

Ser Arg Lys Leu Leu Gly Lys Lys Arg Tyr His Pro Ile Gly Gly Thr 35 40 45

Val Phe Asn Gln Leu Leu Asn Phe Tyr Arg Leu His Asp Tyr Met Ala 50 60

Asp Leu Ala Gly Lys Tyr Lys Thr Tyr Arg Leu Ile Ala Pro Phe Arg 65 . 70 . 75 . 80

Thr Glu Val Tyr Thr Ser Asp Pro Ala Asn Val Glu His Met Leu Lys 85 90 95

Thr Asn Phe Glu Ser Tyr Gly Lys Gly Pro Tyr Asn Cys Ser Ile Leu 100 105 110

Gly Asp Leu Phe Gly Glu Gly-Ile Phe Ala Ile Asp Gly His Lys Trp

•	i.	115		i que. Estas			120		,		1 121	125	10			:		: .	· ··	
۸	c 1 $\frac{n}{2}$	^\ ^\	1 2 1 2 1 mm ³¹	l para	Val-		Con	Love	/ / / / C L	DL -	964 48 Carly)。***1197. T L	in die Annei	}⊹; Vol∷	i an	7				
Arg	Glu 4	77.	1 1 2 2 2 2 2 2	3 68 B 30	3.0	1257	1 : 1	100	40.00	2 5 .	1.40 %	2 1	100 CV		sale are en			umi 188		
	100)	h i	; ;	Lagari		7388	5.15		 1961) (8	I	1407	i na siya	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		nara, s Haran					
Arg	Asp 🗥	lvr	Ser	Ser	lle:	val -	Phe :	Arg	ľvsí	Asn	Ala	Val⊡	Arg	Leu	Ala:			775 p		
$14\overline{5}$	1,1	7G 37		1.4.5	150∵	66.1%	1 to 1 to 2	10.	ንድንጀ	155	18847 36	(i,i,j)	ist jirya		160	٠.	· .	700	٠,٠٠٠	
															42.					
Lys	He,	Leu	Ser	Gly	Ala	Ala	Thr	Ser	Asn	Gln	Pro	Val	Asp	lle	Gln ·		1.5	ar ja	•	
	139	an mi di n	oogra u aes buza	165	1 425 3 425	d MEDIS Nova i	13.13	- MG(2)	170	rid L	HERONE		11) (1) 10 (5)	1/5	भाग्रहाम	$4 \cdot (1)$	(5)[4] - ·	RMI	100	
Acn	Loui	Pho	Mot	ariei. Laro	Cons	<i></i> գութ. Մեթ ր	Dhàt	Acn.	Kaan Coni	608 11a	Conw	rasiv. Clin	υ β' Vol.) (13/36) 	Louise		(3.2.2) (3.2.2)	alar -	\$1.374	
ysh	Leu	Hen:	180	rys	re are	1111 5 944 4	ा मुख्य इन्द्रिक्ट	185.	261	1.16	3615.	ulus astro	100.	Ala	nlia nlia		583 j 656 j	, , , ,	1 337 1	
	Q.	H H	100 11 [].	si)f	1	3343	to by	100°	oros.	8-13	erani. Prattin	ander of Antonia	1.50 tr	asta : 34 - 725		3 14 1 14	7 3 ·	nin di	i i Historia	
Gly	Val:	Glu"	Leu-	Asp -	Ser	Leû®	Gly:	Gly	Ser	Asn	/Glu≥	Glu:	Glv.	Ala-	Lys	\$ B	$\Im x +$	115	213	
-	ារដូវ	195¢		医原性 医	3.2	再的表页	200%	. 1500	58.54°	177	8624F	205	1.7 -43	216.374	4.1254	, ,	81.4	1,70	1.34	
	7.2		Man.	455 o	i si	Fiag	asin I	115 /1	計劃部	BHA :	alis:	1913.73	⊴ਂ ੪	j. 14 .	<u>Pe</u> rtin t	; · · ,	કાનું છે.	AUG.	180	
Phe	Ser	lle	Ala	Ala	Asp	Asp	Val	Ser	Met	Arg	Thr	Leu	Trp.	Arg	Tyr.:	.z - 45	1.57	317	ja er	
	210	3 E (1) 2 E (2)	はおおい	1.454 (A)	ar Dil	Z153	PERMANANTANAN PERMANANTANAN PERMANANTANAN PERMANANTANAN PERMANANTANAN PERMANANTANAN PERMANANTANAN PERMANANTANA	- 55%	SET A	。李成	220	ir Harst.	រៀវ ន		rith.	r B	ORVE)	99113	\$86	
Val	Ach	Valle	arayan Tanan	Tnn	u aa T uo t	Tau:	Correction I	Anin	Alor	(12) 1 1: 011	ospeciel Ann	$W_{\bullet}V_{\bullet}$)6) - 6)) .O.L	} (}.() .() on .	Glu		302	1743年	DHC.	
225	W2h	Vair	Leu″ SXX7	411 9) 4005	53U.	Leu	Lys:	Arg	Alas	235	ASII .	vai	ULY	Ser.	240		3 (33.): 3 3	THE .	178 211	
<i>LL</i> 0	000	11 1	acigs.	go tu	9-19	flyt	ous.	302.15	Seco	REAL I	netue	reación Referirs	₹\$ -124 115 - 211	9 49 66 2920-66	, 240 ,3 5 <u>8</u> 666	egi inga Ngjarag	enar Bern	((200 €) 1 (200 €)	(1 : :::	
Ala	Lys	Leu	Lys	Lys	Ser	Leu	Gln	Val-	Val	Asp	Glu	Phe	Val	Tyr	Lvs	a 191 1. 18	area eq.	4 74 4 14	ме ў (1711)	
	•		•	245					250					255				, ,	. , -	
	.,		_		m)										_					
Leu	lle	His		Arg	Thr	GIn	Gln		Asn	Met	Pro	Gly		Asp	Ser		100			
			260					265				•	270				موسد در ماند	12. 1		
Val	Met	Gln	Lau	Lvc	Tve	Aen	Aen	Ha	Lou	Son	Ana	Pho	Loui	Cln	Laus					
Yaı	MCr	275	Leu	Lys	цуs	nsp	280	116	beu	261	AI g	285	Leu.	GIII	Leu	*1.61.1	,	11.5		
		210				•	200											275		
Thr	Glu	Ala	Thr	Pro	Lys	Tyr	Leu	Arg	Asp	He	Thr	He	Ser	Phe	Ile:	. .				
	290					295		_	-	٠.	300									
						m :		m 1	mı	_	,		ъ.		_		•	•	٠.	
	Ala	Gly	Lуs	Asp		Thr	Ala	Thr	Thr		Ser	Trp	Phe	He						
305					310					315					320					
Mot	Leu	Care	1 770	Tur	Pro	Hic	Val	Cln	Clar	Lvc	Vol	Clu	Cln	Clar	Ho					
MEL	Leu	Cy S	Lys	325	110	1112	Yaı	UIII	330	гуз	Vai	uru	UIII	335						•
				000					000					000						
Lys	Asp	Ala	Thr	Gly	Cys	Lys	Glu	Val	Ala	Asp	He	Ser	Glu	Phe	Ser					
•	· -		340	-	٠.			345		-			350							
	_	,			.			a .				_	_							
Ala	Cys	Val	Thr	Glu	Gļu	Ala		Gly	Lys	Met	His		Leu	His	Ala					
		355					360					365								
110	Leu	Thr	Chi	This	Lou	Ara	ΠΔ	Tun	Pro	۸۱۸	Vol	۸۱۵	Va I	Aan	110					
nia	370	1 111	uru	1111.	1.cu	375	116	ıyı	110	ліа	380	nia	Val	wsh	nia					
	010					0,0					000		•							
Lys	Gln	Cys	Leu	Cys	Asp	Asp	He	Met	Pro	Asp	Gly	Phe	Ser	Val	Lys					
385				•	390	•				395					400					
				,, ,		m	٥.	_		, .										
Lys	Gly	Asp	Met		Ala	Tyr	Gln	Pro			Met	Gly	Arg		Lys					
				405					410					415						
Sar	He	Trn	Glv	Asn	Asn	والا	Glin	Clo	Pho	lve	Pro	Gla	Ana	Trn	Lau		,			

									25/35)						
٠			420					425					430			
Asp	Lys	Asn 435	Gly	Cys	Phe	Gln	Gln 440	Ala	Ser	Pro ·	Phe	Lys 445	Phe	Thr	Ala	3.0 (G):
Phe	Gln 450	Ala 	Gly	Pro	Arg	Leu 455	Cys	Leu	Gly	Lys	Glu 460	Phe	Ala	Tyr	Arg	•
Gln 465	Met	Lys	lle	Phe	Ser 470	Ala	He	Leu	Leu	Arg 475	Phe	Phe	Thr	Met	Lys 480	
Leu	Ser	Asp	Glu	Arg 485	Lys	Thr	Val	Asn	Tyr 490	Arg	Pro	Met	Leu	Thr 495	Leu	
Leu	lle	Asp	Gly 500		Leu	Ile	Val	Arg 505		Phe	His	Arg	Met 510	Asp	Glu _.	•
Lys	Thr	Ala 515		:	· :	. ;}		• •		14		, '	•			
			••			\$ 57	11.13						10 p	• • •		
<210 <211 <212 <213	> 34 > DN	l IA	icial	l Sec	uenc	: :::	•	j :	: 1		#	i E		* <u>†</u> . = 3	. '	
<220 <223	> > De	scri	iptic	on of	Art	ific	ial	Sequ	ience	: Ar	tifi	cial	ly		· · · · · · · · · · · · · · · · · · ·	
<400 tgga	_		ctcat	tagag	st ac	tcaa	ıaaac	gct	:t							34
<210 <211 <212 <213	> 24 > DN	l A	icial	Sec	Juenc	сe										
<220 <223	> De	scri	ptic esize	on of ed Pr	`Art imer	ific Seq	ial Juenc	Sequ	ence SiP18	: Ar 9-Nc	tifi o-RV	cial	ly			
<400 gcaa			acca	itggt	g tt	ct										24
<210; <211; <212; <213;	> DN	A	cial	Seo	uenc	e										

<220>
<223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, GR-SST-RV1

<400> 63

The state of the contract of the second

cacatgaacg agacgaactg ggtttgg total that with the part of a few constraints of the competition of the constraint of the constraints. <210> 64 <211> 506 was finished was and system before the system particles and the second system. <2 F2> PRT <213> Sesamum radiatum the South of the South Certification of the South Certification (Certification Certification Certifi <223> SrSiP189 ing a constitution it of the hat her brokens are but but the bid. Met Glu Ala Glu Met Leu Tyr Ser Ala Leu Ala Leu Thr Phe Ala Île Phe Met Val Tyr Arg Ile Leu Ser Asn Ser Gln Glu Lys Ser Ser Leu 12. 30 lle Lys Leu Pro Pro Ser Pro Pro Gly Trp Leu Pro Val Ile Gly His Val His Leu Met Lys Asn Leu Leu His Arg Thr Leu Tyr Asp Phe Ser (并)《经验学院类类者的政治内部中部各种原则的 Val Val Val Ser Ser Ser Leu Val Glu Glu Cys. Phe Thr Lys Tyr 1914 12 85 Asp Ile Val Leu Ala Asn Arg Pro Gln Pro Ser Val Asp Arg Arg Ser 100 105 110 Leu Gly Phe Ser Thr Thr Ser Val Ile Gly Ala Pro Tyr Gly Asp His 115 Trp Arg Asn Leu Arg Lys Leu Cys Asp Leu Glu Val Phe Ala Pro Thr 130 140 lle Ser Ser Leu Tyr Lys Ile Ser Ser Ala Gly Phe Ala Lys Val Asn 165 170 175 Leu Glu Thr Lys Ile Val Glu Leu Thr Phe Asn Asn Ile Met Arg Met 180 185 190 Val Ala Gly Lys Arg Tyr Tyr Gly Glu Glu Ala Glu Asp Asp Glu Glu 195 200 . 205 Ala Lys Arg Phe Arg Asp Leu Thr Lys Glu Ala Leu Glu Leu Thr Ser 210 215 220

Ala Ser Asn Pro Gly Glu IIe Phe Pro IIe Leu Arg Trp Leu Gly Phe Asn Gly Leu Glu Lys Lys Leu Ala Val His Ala Arg Lys Thr Asp Glu 245 250 255 Phe Met Gln Gly Leu Leu Asp Glu His Arg Arg Gly Glu Arg Gln Asn 260 270 Thr Met Val Asp His Leu Leu Ser Leu Gln Glu Ser Gln Pro Glu Tyr 275 280 285 Tyr Thr Asp Glu IIe IIe Thr Gly Leu IIe Val Ala Leu IIe IIe Ala 290 295 300 300 -Gly Thr Asp Ala Ser Val Val Thr Thr Glu Trp Ala Met Ser Leu Ile 305 310 315 Leu Asn His Pro Gln Val Leu Glu Lys Ala Arg Lys Glu Leu Asp Thr 325 330 335 Leu Val Gly His Glu Arg Met Val Asp Glu His Asp Leu Pro Lys Leu 340 Arg Tyr Leu His Cys Ile Val Leu Glu Thr Leu Arg Leu Phe Pro Ser 355 Val Pro Thr Leu Val Pro His Glu Pro Ser Glu Asp Cys Lys He Gly 370 Gly Tyr Asn Val Pro Lys Gly Thr Met Ile Leu Val Asn Ala Trp Ala 385 Ile His Arg Asp Pro Lys Val Trp Asp Asp Pro Leu Ser Phe Lys Pro
405 410 415 Asp Arg Phe Glu Thr Met Glu Val Glu Thr His Lys Leu Leu Pro Phe Gly Met Gly Arg Arg Ala Cys Pro Gly Ala Gly Leu Ala Gln Lys Phe
435
440
445 Val Gly Leu Ala Leu Gly Ser Leu Ile Gln Cys Phe Glu Trp Glu Arg 450 455 460 Met Ser Ala Glu Lys Ile Asp Leu Asn Glu Gly Ser Gly Ile Thr Leu 465 470 475 480 Pro Lys Ala Lys Thr Leu Glu Ala Met Cys Lys Pro Arg His Ile Met 485 490 495 Glu Arg Val Leu Arg Gln Val Ser Asn Val 500

```
<211> 1518
<212> DNA
 <213> Sesamum radiatum
                               <220>
 <223> SrSiP189
                                                   office a first gar and a first the fifth one and given have according to the care
 atggaagetg aaatgetata tteagetete geteteacet tegecatatt eatggtttae 60
agaattettt etaattegea ggagaaaage ageetgatta agetgeegee gageeegeg-120
ggttggctcc cggtgatcgg ccacgttcat ctcatgaaaa atctcctcca tagaacacta, 180
 tacgacttct cccagaaact gggacccata ttttccctcc ggttcggcac ccgcctcgtg 240
atttcgtcgt tgtacaaaat ctcgtccgcc ggtttcgcga aggtgaattt ggagacgaag 540
 attgttgagc tgacgtttaa taacataatg aggatggtgg cggggaagag atactatggg 600
attgttgagc tgacgtttaa taacataatg aggatggtg cggggaagag atactatggg 600 gaggaggcgg aggacgacga, ggaggcgaag, aggttcagg acctgacgaa/ggaggctttg, 660 acctgatgagttgacga gcgcttccaa tcctggtgag atatttccaa tattgcggtg gcttggtttc 720 aatgggttga agaagaagct ggctgtcac gcgcggaaga cggatgagtt catgcaaggg 780 ctgctggacg acccgacg/ggggcgaggcccaagaacacca tggttgatca/tttgctttcg/840 acccgaggaat ctcaacctga/gtactacact gatgaaatca/tcactggcct catagttgca/900 ttgataattg cgggaacgga tgcatcgtt gtaactacag aatgggcgat gtcccttata/960 ctaaatcatc cccaagtact/tgaaaaggct/agaaaagaac/tggacactct/agtaggacac,1020 gagaacgtag gggacaatga/tactggtgc cacacgaacc atcggaggat 1140 tgtaaaattg ggggatacaa/tgtcccaag gggacaatga/tactggtgaa tgcttgggaa/1200
 tgtaaaattg ggggatacaa tgtccccaag gggacaatga tactggtgaa tgcttgggca 1200 atacaccgag accccaaggt gtgggacgac cccttgagct ttaagcccga caggtttgag 1260
acaatgaag tggagacaca caasctstts ccsttcsga tggscassas ascststccc 1320 gsasctsgat tggcscasaa stttstssssittsgatttsgatttsgatttsgatttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgatttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgatttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgattttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgatttsgattsgattsgatttsgatttsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsgattsga
 cctaaagcta agacgttgga agccatgtgc aaacctagac atatcatgga gagagttctt 1500 cgtcaggttt cgaacgtc
 <210> 66
<211> 20
<212> DNA
  <213> Artificial Sequence
  <220>
  <220>
<223> Description of Artificial Sequence: Artificially
                    Synthesized Primer Sequence, NtUBQ-FW
  <400> 66
  ggaatgcaga tcttcgtcaa
                                                                                                                                                                                                             20
  <210> 67
  <211> 18
  <212> DNA
  <213> Artificial Sequence
  <223> Description of Artificial Sequence: Artificially
```

	Synthesized Primer Sequence, NtUBQ-RW	
<400> cctag	67 aaacc accacgga	18
<210><211><211><212><213>	24	
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, SiP189-bam-FW	
<400> ttttc	68 agcca acatggaagc tgaa	24
<210> <211> <212> <213>	24	
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, SiP189-nco-RV	
<400> gcaaa	69 tgatc aaccatggtg ttct	24
<210> <211> <212> <213>	25	' .
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, STAR-LF1	
<400> acgaag	70 sttat gcggccaatt aaccc	25
<210> <211> <212> <213>	25	
<220> <223>	Description of Artificial Sequence: Artificially Synthesized Primer Sequence, STAR-LR1	
<400> ccacct	71 tgacg tcgcggccta atacg	- 25

```
Colon of the Artificial Const.
<210> 72
<211> 24
                                                                                                                                                                                                                                                                                                                                                                                                                 i tori
Martiniana Marana
  <212> DNA
  <213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, M13-47(F)
                                                                                                                                                                                                                                                                                                                                                                      unitrativity and the telephone in the telephone
  <400> 72
  cgccagggtt ttcccagtca cgac
                                                                                                                                           C. Combines of the Computer Section of the Computer Action 18 (18 Computer 
  <210> 73
<211> 24
<212> DNA
<213> Artificial Sequence
                                                                                                                                                                                                                                                                                                                                             STREET CONTRACTOR SOUNTS FOR
  <220>
  <223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, RV-M(R)
                                                                                                                                                                                                                                                                                                                                                  CITED APTATOCHAIT SOCKHOROGO
  <400> 73
<210> 74
<211> 3069
<212> DNA
<213> Sesamun indium
                                                                                                                                                                                                                                                                                                                                               A State of the sta
 tacgtggttg taaattaagg tggcatagtc aaagctgtgt aggatggagg aattagacac 60 ttccccagtc ccccacagac tattcccgag ctgaccaaac acagtcgaaa gtgtggggcc 120 caatgaaatt gacagatgac gtctagtgta gtgtgaatgt gtgatatttt tgcagaatat 180 tgtaaaagag ggttcaccaa atctcactag tttgtgacta attgactatt tttgcagaaa 240 attcgtattt agtatagggt cttggtcaaa ttaattaatt atataacaaa tgtgatatat 300 ttaatttgtt attaattttt ttatatttgt tgtgtaatta gttaggattt tatataagaa 360 tttgaaaaaa tgagatgtt ttttgtaaat caaattacac aatatcatgt attgggtttt 420
    tegteetgaa gtegettgaa aattgattag ateggeggae ttgaacagae gagtgaatgg 480 acatgattta aaattttaag gataaatata tatagtatea gttateaaaa taaaaaattt 540
  cetteaaaat eatggettg tttaagatag ttttttgagt aatgtggeac cataatteec 600 aageactaga agtgeaattg taaateeaac ggtacetagt ttaattgata aaattaaagt 660 ceaaaaattt teetgagaaa eeaattegag eaagggtaca teaaaggtge eaceagggag 720 ttaageaaga aatgteeet aaactttagg eatgaggtat eeetaaaa taaattgaec 780 taaaaagatt eaaatggett agagtegaga aaaagactaa gtagaceatt agggaageee 840
  acatectaa gatcetcag cegaagtaga ggeetatgeg geagteagee tagtgaettg 900 ggatteeeta getetgaaag aattaatatt gteecaagaa tetaaggeta catagtagaa 960 atgaaaacaa agegaatta aatttgaage cageatgatt gaatttttt tttttttt 1020 aggtgtttaa geacteaaca atgtacaata aataaacgtg tggetaattt aaagaacatt 1080 gaaagetgge caagaattat acettttaaa gegagtggag ttteegatgt ttgageteet 1140 atteaateeg teaatagaa eggeteetttt aatggtatee aegataeett 1200
  tgtcgagggg atttctcgtc tccttgctag aggattcaat attaccaagg ggtcaaaact 1260 atactaactt aaagaagatt gagaacacac tattaaattc tcgatcccaa ttttcaagcc 1320 tttgcaccta gttgaaagct tgtgcgtaga gatgcttttg agagagtgtc ggggaggaga 1380 ggggatggaa cacaaaattt taggcttatt ttttcttttt ttttttgtc aaaaatgtct 1440
```

```
ctgttaaagt tttgtgcatg tcctctatat gccaaatatt tggtggtaag cacgacaaag 1500
gtatgccaaa tgaagttgta ttaactatgt tgaataagat ggtcctatac taatagatta 1560 cataggccaa cccattagct tgtaggtcac atattccaac ataatgtaga ggtctaagca 1620
 caagcagacc catgccatat ggcgtccatg gggtagtcca ggtgatattg acgtaagttc 1680 ttttaagcca catcaacaaa cttcagccgt ccaagcaagg acatgtggcc gcctcaaaag 1740
 aaggeeteaa tgetteetta teeetaaaac aactetaget ttggaaacca gateagatga 1800
 ggatatecee taagetattt caaaaaatet aggaacetta tetgtageag aetttgttaa 1860
 tttttcaaat caagggactc caacagccaa gcgataaccc tcaccaaatt tgtgaaggat 1920
tcgatattat ccaaccagtt gatgatttgc ttataaagtg caatcttccc ccaacaaaaa 1980 agccaattcc aacttttact ttcaaattat agctttaatt tctgacttaa aatttcatat 2040 tataaatttc aatctcttaa gtgtacacaa aatacaagat atttcactct tttgtatttt 2100 tctaattccc ataattttat ctttattttg tattttgatt gaacccgagc acatctttga 2160 cttgcatcaa caatattagc tctaaattaa acatagaatt taatgttaaa atgagaaaag 2220 gaactcatac agatcggact caaaacctta acacctaata aagtatgcat cctaataaaa 2280 agttatacc aaagtagaat taatgagaat taatgagaat taatgagaata 2280
agttattacc aaagtgaaat tatgcttaat gaaaatcgaa atcagaagta gttcttaatt 2340.
ggagagtttc gagacggcaa gaatattgca actcatcctc acacctaccc atctatttca 2400
tactettaaa ttataateta atteaatata cacaacaace tateacatta atatacaata 2460
 tgaaaggtca ataaaatatt tacgctggca aacctcccca gtagaattcg ggcacatatg 2520
aagtgttaac cattcaaata tggacaaagg aacactagag acacgaagtt tatttcaaag 2580 gaaaattttg tctaaaattg aatttaatta aatttaaatt aattatata taaatataat 2640
gtattttaca tcatgattga tatataattt taaaaaaaat aattattcca actattaaca 2700 ttaattaata aataactttt acaagaccca ggccaccaac tcccgtccac atgaaagaat 2760
gggtaaccgc taagtctata ttttagtact acgacgtatg caaatacgct ttttccacaa 2820 aaatcaaatt ttaattttta ctttatccaa ggcaagaaaa caaaaaatgc ataaattcac 2880
gttctaattc atcaatactc aagaaatagc atacttgatt tgaactgaga tttgtcactt 2940.
tcctacaaat tctgcagact atgaaaacga catcaaccaa ccaatatcca ctctctatat 3000
aaatagcatc acttcactag caatttctca tcaactcata gagtactcaa aaacgctttt 3060 ...
                                                                   The state of the s
tcagccaac
<210> 75
                                                                                                                                                                  200 B
```

<220>

aatgaaattg acagatgacg tctagtgta 29

<210> 76

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<400> 76 ctgcgaatta gaaagaattc tgtaaaccat

30

<211> 29

<212> DNA

<213> Artificial Sequence

<223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, gSST-FW1

<223> Description of Artificial Sequence: Artificially Synthesized Primer Sequence, gSST-RV2

```
<211> 2815 care <212> DNA a mass for the standard of the stand
aatctctcta gttcgtgatt atgactattt ttgcagaaaa tttgtattta gtttagggtt 120
ggtaaaatct, aatttataga gtaaatatga tgtatttatt, ttgtgattga ttacttttat 180
atttattgta taattagtta taatttgata aagtgtgata tttttataa attagattac 240
atattattat gtactgagttattcgttctg atgccattta aaaattggtt aggtcggcga 300 con
cttgaactga; cgagtgaagg gacttgattt; aacattttaa; ggatatatatatatatatatatacc; 360, g in c
agttatcaaa ataaaagttt tettteaaaa teatagtttt gtttaagata attttgtgag 420
 tatatgttgc,accacaattc,ccaagcacta,taagtgcaac,tgtaggtcta,attggaccta,480,
gtttagttga caaaattgaa gtccaagaat atcttcaaga agccaattcg tgtaatggta 540
cgtcaaaggt gccaccaggg aatcaagtag gaaatttccc ctaaatgtta ggcatgaggt, 600 gccactataa agaaaattga cccaaagaga tacaagtatc ttagagtcga gaagaagact 660 gcc
acgtagacca ttagggaagt ccacatgcct, aagattetge agetgaagca caggectagg 720 135.
 tacggtcagc ccagggactc gagatcccct agetctcaaa gaattggtat tggcccagga 780
 atctaagget acatagcaaa aacgaaaata aaacaaactt aaatttgaag tcaacgggat 840
 tgaatcctat tttctcgggt gttcaaactc aagcatgtaa aataaataaa cgtgtgacta 900
 atttacaaaa cactgaaaac taattacaaa ttatacctta aaagcatgtg tagttttaa, 960
 cgtttgagct ttcgtcaatc cattcacgta gagataaacg gacgtctcct ctaagggtat 1020
 ccacaatacc; attggcgagg agatttcttg tctattagag gattcgagat taccatggag, 1080 ttagaactat aaacctaaag aagatcgaga aaatactatt agattagtgt tctcaatctc 1140
aatteteaag cetteaaace tagttaaaag ettgagaaaa tttgtgegta gatatgttt 1200 ggagagagtg teggagagaa gaggggateg ageacaaact ettageeta ttetttete 1260 ttettgeeg aaaaatgtet ttgttagagt eettgtgeat gttttetata tgeeaaatat 1320
 gtggtggtaa gcacaacaaa gttatgtgaa aagaaattgt attagcacta cgttgaataa 1380
 gattgtcttc tactaataga tgatagaggg caaccattgg cttgtcggtt acttattcca 1440
 acataatgta gaggcccaag catgataaga cctatgccac aggacgtcct tgggtggtcc 1500
 aagtgatatt gacgtaagac cttttaacct actteggeag getttageea taaccteeag 1560,
 cetytyaaac eegateagat gaggatatee eeteageeee teeaaaaate taggaatete 1620 km
 atccgcagca gatttcggta tcttttccta gaagatcaaa aaactctaac cactaagaga 1680
 taacccccc cacaaatta atggaaaatt tggccttatc taactggcta ataggttgcc 1740
 cataaattgc gagctcccc aacataaaaa gccaatccaa ctttactttt aaattatagg 1800 tttagtttct aacttaaaat ttcatattat gaatatcaac ctcttatgta tacacaaagt 1860 aacaagatat tttactcatt tgttttctct tagttcctat aatttatct ttcttgcatc 1920 aacaatattt gctctaaatt aaatatagaa tttaatgtta aaatgagaaa acggactcaa 1980 aaccagaaca cctaataaag tatgcatctt aataaaagt tattacgaag gagaaaaata 2040
  tgcttaataa aaatcgaaat cagaagtagt tcttaattgg agagtctgaa aacggcaaga 2100
 atattgcaag tcatcctcac tttctcatcc atagacagtc acacctaccc cacatatttc 2160
  atactittaa attattatet aatttaatat aegeateant teataatata taataegaaa 2220
 ggttaataaa atatttacgc tagcaaactt cttcagtaga attcatgtac ataagaagtg 2280 ttgaccattc aaatatggaa aaagaaacac tagagataag aaacttagtt gtgaagcaga 2340 aaatattaa gttggttggt tggatttgaa ctaattaata taataaatat aatatatcgt 2400 gtaaattgaa aaacgactat taacatcaat taataaataa ttttctgtta gtgaaggatgg 2460 actacaagac ctaggccacc aacccccatc cacctgaatg aatgggtaac cgctaagtcc 2520 atatttcagt actccggcgt ctgcaaaaac gctttttcca caaaaatcaa attttaagtt 2580 tttactttat cctaggcaag aaaacaaaat atgcatagat tcacgtcaa attcatcaat 2640 gctcaagaaa tagcatactt gatttgaac gagatttgtc actatcctac aaattctgca 2700 cactatgaaa acgacatcaa ccaaccaaga tagcatctct ataaaatacaa tagcatgat 2760
  cactatgaaa acgacatcaa ccaaccaaaa tccactctct ataaatacca tcacttcact 2760
  agcaatttct catcaactca taacgtactc aaataaacac gctttttcag ccaac
```

<210> 78 <211> 507 <212> PRT

<213> Sesumum alatum

<400> 78 Met Glu Ala Glu Met Leu Tyr Ser Ala Leu Ala Leu Thr Phe Ala Ile 10 15 lle Met Val His Arg Ile Leu Ser Asn Ser Gln: Asn Lys Arg Ser Leu 20 25 30 Ile Asn Leu Pro Pro Ser Pro Pro Gly Trp Leu Pro Ile Ile Gly His Leu His Leu IIe Lys Asn Pro Leu His Arg Thr Leu Tyr Asp Cys Ser 50 55 60 Gln Lys Leu Gly Ser Ile Phe Ser Val Trp Phe Gly Ser Arg Leu Val 65 70 75 80 Val Val Val Ser Ser Ser Ser Leu Val Glu Glu Cys Phe Thr Lys 85 90 95 Asp Ile Val Leu Ala Asn Arg Pro Asp Leu His Leu Asp Leu Arg Ser 100 105 110 Leu Gly Ala Ser Thr Ile Ser Val Ile Gly Ala Pro Tyr Gly Asp His 115 120 125 Trp Arg Asn Leu Arg Lys Leu Cys Asp Leu Glu Val Phe Ala Pro Thru 130 Arg Leu Ala Ser Phe Leu Ser Ile Arg Arg Asp Glu Arg Asp Arg Met 145 150 155 160 Ile Ser Gly Leu Tyr Lys Ile Ser Ser Ala Gly Leu Ala Lys Val 165 170 175 Leu Glu Ala Lys Ile Ala Glu Leu Thr Phe Asn Asn Leu Met Arg Met 180 185 190 Leu Ala Gly Lys Ile Tyr Tyr Gly Glu Glu Ala Glu Asp Glu Glu Glu 195 200 205 Ala Lys Arg Phe Arg Asp Met Thr Lys Glu Ala Leu Glu Leu Met Asn 210 215 220 Thr Phe Asn Leu Ala Glu IIe Phe Pro IIe Leu Arg Trp IIe Gly 225 230 235 Asn Gly Phe Glu Lys Gln Leu Pro Val His Ser Arg Lys Thr Asp 245 250 255 lle Met Gln Gly Leu Leu Asp Glu His Arg Arg Gly Glu Arg Gln Asn 260 265 270 Thr. Met Val Gly His Leu Leu Ser Leu Gln Glu Ser Gln Pro Asp Tyr 275 280 285

Tyr Thr Asp Glu Ile Ile Thr Gly Leu Ile Ile Ser Leu Ile Ile Alams

Gly Thr Asp Ala Ser Val Val Thr Thr Glu Trp Ala Met Ser Leu Leu 305 310 315 320

Leu Asn HistPro Lys Val Leu Glu Lys Ala Arg Gln Glu Met Asp Three 325 330 335

Leu Val Gly His Glu Arg Met Val Glu Glu Asp Asp Leu Pro Lys Leu 340 345 350

Arg Tyr Leu His Tyr He He Leu Glu Thr Leu Arg Leu Phe Pro Service 355

Val Pro Thr Leu Val Pro His Glu Pro Ser Glu Asp Cys Asn Ile Gly 375

Gly Tyr Asn Val Pro Lys Gly Thr Met IIe IIe Val Asn Ala Trp Alassi (1) 1 385 390 395 400

Ile His Arg Asp Pro Lys Val Trp Asp Asp Pro Met Ser Phe Lys Pro Lys 405 410 and 415001

Asp Arg Phe Glu Thr Leu Glu Val Glu Thr His Lys Leu Leu Pro Phesiologica 425 425 430

Gly Met Gly Arg Gly Cys Pro Gly Ala Gly Leu Ala Lys Lys Phe 435

Val Gly Leu Ala Leu Ala Ser Leu Ille Gln Cys Phe Asp Trp Glu Arganomo de 450 455 460 460 Gli Francisco de 1880 Arganomo de 18

lle Ser Ala Glu Lys Ile Asp Leu Lys Glu Gly Ala Ser Arg Ile Thr 465 470 475 480

Leu Pro Lys Ala Thr Thr Leu Glu Ala Met Cys Lys Pro Arg His Val 490

Met Glu Lys Yal Leu Arg Gln Val Ser Asn Val

<210> 79 <211> 1524

<212> DNA

<213> Sesumum alatum

<400> 79

atggaagetg aaatgetata tteagetete geteteacet tegecataat eatggtteae 60 agaattettt caaatteaca gaacaagege ageetgatea atetgeegee gageeegeet 120 ggttggctgc cgattatcgg ccaccttcat ctcataaaaa atccactcca tagaacacta 180 tacgactgct cccagaaact gggatccata ttctccgtct ggttcgggtc ccgcctcgtg 240 gtgstgstgt cetecteete etgstgsag gaatgtttea ceaagtaega eattgtettg 300 gecaacegee etgaceteea tetgsacetg egateacteg gggceageae eateagegta 360 ateggggeee ettaegggga eeactgege aacetgegaa agttgtgega tettgaagta 420 ttcgccccga cccgtctcgc ctccttctta tccatcagac gagacgagag ggaccgcatg 480

•			,			
atttccgggt	tatacaaaat	ctcgtcggcc	ggtttggcga	aggtgaattt	ggaggcgaag	540
attgcggagc	tgacgtttaa	taacttaatg	aggatgttgg	cggggaaaat	atactatggg	600
					ggaggctttg	660
					gattgggtgc	720
					catgcaaggg	780
					tttgctttcc	840
					cataatttca	
ttgataatcg	cggggacgga	tgcatccgtt	gtaactacag	aatgggcgat	gtctctttta	960
ctaaatcatc	ccaaagtact	tgaaaaggct	agacaagaaa	tggacacgct	ggtaggacat	1020
gaacgcatgg	tcgaagaaga	cgatctcccc	aaactacgtt	accttcacta	cataatcttg	1080
gagaccttaa	ggttattccc	ttctgttcca	acgttggtgc	cacacgaacc	gtcggaggac	1140
		cgtccccaag				1200
		gtgggacgac				1260
acattggagg	tggagacaca	caagttgttg	ccatttggga	tgggcaggag	aggttgtccc	1320
ggagctggat	tggcgaagaa	gttcgtggga	ttggctttgg	catcgctgat	ccagtgcttc	1380
gactgggaga	gaattagtgc	cgagaaaatt	gacttgaagg	aaggtgcttc	taggataacc	1440
		ggaagccatg	tgcaaacctc	gacatgtcat	ggaaaaaagtt	1500
cttcgtcagg	tttcgaacgt	ctga.				1524

This Page is Inserted by IFW Indexing and Scanning Operations and is not part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:
☐ BLACK BORDERS
☐ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
☐ FADED TEXT OR DRAWING
DELURRED OR ILLEGIBLE TEXT OR DRAWING
☐ SKEWED/SLANTED IMAGES
☐ COLOR OR BLACK AND WHITE PHOTOGRAPHS
☐ GRAY SCALE DOCUMENTS
LINES OR MARKS ON ORIGINAL DOCUMENT
\square REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.